

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: December 14, 2003, 06:55:31 ; Search time 22 Seconds

(without alignments)  
1400.105 Million cell updates/sec

Title: US-09-836-392-21

Perfect score: 3822

Sequence: 1 MLRLRATDAMKNFSEFRQ.....IFYQSYELGRLKTRKR 728

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.rep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.rep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.rep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.rep.\*  
5: /cgn2\_6/ptodata/2/1aa/6C.COMB.rep.\*  
6: /cgn2\_6/ptodata/2/1aa/6D.COMB.rep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	275.5	7.2	394	US-09-345-473E-19	Sequence 19, Appl
2	244.5	6.4	823	US-09-886-319A-63	Sequence 63, Appl
3	243.5	6.4	505	US-08-222-616-20	Sequence 20, Appl
4	243.5	6.4	505	US-08-446-648-20	Sequence 20, Appl
5	243.5	6.4	505	US-08-492-723-2	Sequence 2, Appl
6	243.5	6.4	505	PCT-US95-04228-20	Sequence 20, Appl
7	243	6.4	455	US-09-221-235-5	Sequence 5, Appl
8	243	6.4	455	US-09-221-928-5	Sequence 5, Appl
9	243	6.4	455	US-09-221-928-5	Sequence 5, Appl
10	243	6.4	455	US-09-221-236-5	Sequence 5, Appl
11	243	6.4	455	US-09-221-416-5	Sequence 5, Appl
12	243	6.4	455	US-09-221-245-5	Sequence 5, Appl
13	243	6.4	455	US-09-163-115-5	Sequence 5, Appl
14	243	6.4	455	US-09-221-528-5	Sequence 5, Appl
15	243	6.4	455	US-09-593-553-5	Sequence 5, Appl
16	243	6.4	455	US-09-221-237-5	Sequence 5, Appl
17	243	6.4	455	US-09-399-588-2	Sequence 2, Appl
18	241.5	6.3	506	US-09-426-509A-6	Sequence 6, Appl
19	241.5	6.3	511	US-08-232-585-6	Sequence 6, Appl
20	241.5	6.3	511	PCT-US95-05008-6	Sequence 6, Appl
21	238	6.2	800	US-08-469-537A-72	Sequence 72, Appl
22	238	6.2	800	US-08-469-537A-72	Sequence 72, Appl
23	236	6.2	937	US-08-469-537A-105	Sequence 105, Appl
24	236	6.2	263	US-09-035-706-5	Sequence 5, Appl
25	236	6.2	263	US-08-955-841-5	Sequence 5, Appl
26	236	6.2	263	US-09-390-425-5	Sequence 5, Appl
27	236	6.2	263	US-09-566-906-5	Sequence 5, Appl

28	236	6.2	821	1	US-07-928-464-2	Sequence 2, Appl
29	236	6.2	821	1	US-08-003-311B-2	Sequence 2, Appl
30	236	6.2	821	1	US-08-261-432-2	Sequence 2, Appl
31	236	6.2	821	5	PCT-US93-07347-2	Sequence 2, Appl
32	233	6.1	795	3	US-09-031-563-23	Sequence 23, Appl
33	233	6.1	795	3	US-09-392-277-23	Sequence 23, Appl
34	233	6.1	795	3	US-09-258-000-23	Sequence 23, Appl
35	231.5	6.1	822	4	US-09-886-319A-64	Sequence 64, Appl
36	230	6.0	855	4	US-09-417-197-111	Sequence 11, App
37	228.5	6.0	579	4	US-09-529-279-4	Sequence 4, Appl
38	228.5	6.0	579	4	US-10-158-895-4	Sequence 4, Appl
39	228.5	6.0	590	4	US-09-529-279-15	Sequence 15, Appl
40	228.5	6.0	590	4	US-10-158-895-15	Sequence 15, Appl
41	228	6.0	296	2	US-08-701-191A-29	Sequence 29, Appl
42	228	6.0	668	1	US-08-205-018A-2	Sequence 2, Appl
43	228	6.0	859	1	US-08-395-880-2	Sequence 2, Appl
44	228	6.0	859	1	PCT-US95-02792-2	Sequence 2, Appl
45	224.5	5.9	943	2	US-08-469-537A-107	Sequence 107, App

## ALIGNMENTS

```
RESULT 1
US-09-345-473E-19
; Sequence 19, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: NO. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/185781
; CURRENT APPLICATION NUMBER: US/09/345.473E
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 19
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-473E-19

Query Match      7.2%; Score 275.5; DB 4; Length 394;
Best Local Similarity 31.3%; Pred. No. 9.2e-18;
Matches 78; Conservative 42; Mismatches 92; Indels 37; Gaps 8;

QY      3 RHURATDAMKNFSEFRQASMLHALQPCIVAGISIH- LCFALDELAPSSINTVL 60
DB      33 RHDPDEDISQTEIVRQKALFAMLKHPNIIALRGVCLKEPNLCVMEFARQGPLNRVL 92
QY      61 ENADSSFTPIGHMLTQKI-----AYQASGLATLHK-- NTFCDLKSNDIWLSTL--- 110
DB      93 -----GKRIPIIIVNMAVOIARGMNVLHDAIVPIIHRDLKSNIIILIOKVEN 141
QY      111 -DYKEHINIKLSDYGISRQSFHEGALGVEGTPGYQAPRIPIVDEKYMFSYGVLYE 169
DB      142 GDLSNKKI-LKTTDGLARBNHRTTKMSAATYMAPEVIRASMFKSGDVSYGLTWE 200
QY      170 LLSCGRPALGHQIQI-----KLSGKIPVIGQPEVQFRRLQLLMNECWDTRKXP 224
DB      201 LLTEVEVFRGIDGLRIVGVAMNKLALPIFSTCEP-----FAKLMDQWNPDPHSRP 253
QY      225 LALSVSOM 233
DB      254 SFTNIDQL 262

RESULT 2
US-09-886-319A-63
; Sequence 63, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
```

APPLICANT: Halle, Jorn-Peter  
APPLICANT: Regenbogen, Johannes  
APPLICANT: Goppelt, Andreas  
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for  
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound  
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically  
TITLE OF INVENTION: Active Substances  
FILE REFERENCE: 50125/014002  
CURRENT APPLICATION NUMBER: US/09/886,119A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: US 60/222,081  
PRIOR FILING DATE: 2000-08-01  
PRIOR APPLICATION NUMBER: DE 10030149.5  
PRIOR FILING DATE: 2000-06-20  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 63  
LENGTH: 823  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-886-319A-63

Query Match 6.4%; Score 244.5; DB 4; Length 823;  
Best Local Similarity 32.6%; Pred. No. 3e-14;  
Matches 77; Conservative 37; Mismatches 85; Indels 37; Gaps 10;

QY 16 EPRQASMLHALQPCIVALLIGISI--HPLCFALBAPLSSINTVLSERNADSSFFILGH 73  
DB 605 KFLQEKIKIKQYDHPVIVLIGVCTQROQVYIMELVPGSDFLFKRQDELKQL-- 662  
QY 74 MLTQKIAYQIASGLAVLHKNNIFCDLKSNDILWLSLVKEHINIKLSDYISROSFFHG 133  
DB 663 ---VRFSLVAAAGMLYLESKNCIHRDLAARNCL-----VGNNITLKI:SDPMSQ--EDG 712  
QY 134 AGVGEETPG-----YQAPETPRIVYDEKVDMSYGMVLYELLS--GQRPALGHQLOI 185  
DB 713 --GVYSSGKLKQIPKMTAPFALNYGRYSSESDVWSFGILLMETFSLGVCPYPMNTNQA 770  
QY 186 AKKLSKIRPVLGQ--PEEVQFRRLQALMMECWDTPKPKRP-----LALSVSQOM 233  
DB 771 REQVGRGYMSAPQNCPEEV-----FTIMKCMQDKPENRKPFDLHKLIVLYIKM 821

## RESULT 3

US-08-222-616-20  
Sequence 20, Application US/08222616  
Patent No. 563177

## GENERAL INFORMATION:

APPLICANT: Bennett, Brian D.  
APPLICANT: Goeddel, David  
APPLICANT: Lee, James M.  
APPLICANT: Matthews, William  
APPLICANT: Tsai, Siao Ping  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,616  
FILING DATE: 4-APR-1994  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/00586  
FILING DATE: 22-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/826935  
FILING DATE: 22-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 821P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 505 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-222-616-20

Query Match 6.4%; Score 243.5; DB 1; Length 505;  
Best Local Similarity 30.5%; Pred. No. 1.7e-14;  
Matches 75; Conservative 49; Mismatches 77; Indels 45; Gaps 11;

QY 15 SEPRQASMLHALQPCIVALLIGISI--HPLCFALBAPLSSINTVLSERNADSSFFILGH 72  
DB 272 NDLREAOIMGNLHPKLIQIYAVCTEDPIYITELMRGSIQBYL--QNDTSKI----- 326  
QY 73 HMLTQKI--AVQIASGLAVLHKNNIFCDLKSNDILWLSLVKEHINIKLSDYISR--- 127  
DB 327 -HLTQVMAQVAGMAVLESRYIHRDLAARNVL-----VGEHNIYKVADGLARVTK 380  
QY 128 -----QSFHEGALGVGTRPGYAPETPRIVYDEKVDMSYGMVLYELLS--GQRPALG 179  
DB 361 VDNEDIYSRHEIKLPKMT--APPAISNKFSTSDVWSFGILLMETFSLGVCPYPMNTNQA 436  
QY 180 HHQLIQAKLSKIRPVLGQPEEVQFRRLQALMMECWDTPKPKRP-----LALSVSQOM 239  
DB 437 MTGAQVIGMAQNR--LPQSPNCP--QGFNIMLEGNAPKRP-----PTFR 481  
QY 240 TPRMEL 245  
DB 482 TLRWEL 487

## RESULT 4

US-08-446-648-20  
Sequence 20, Application US/08446648  
Patent No. 631302

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
APPLICANT: Bennett, Brian D.  
APPLICANT: Goeddel, David  
APPLICANT: Lee, James M.  
APPLICANT: Matthews, William  
APPLICANT: Tsai, Siao Ping  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: winpatin (Genentech)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,648  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/222616  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0821P3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 505 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-446-648-20

Query Match  
Best Local Similarity 30.5%; Pred. No. 1.7e-14;  
Matches 75; Conservative 49; Mismatches 77; Indels 45; Gaps 11;

QY 15 SEPRQASMLHALQHPCTVALIGISI--HPLCFALSLAPLSLNTVLSENARDSSFTPLG 72  
DB 272 NDFLEAQIMKRLRHKTLQLYAVCTLEDPYITTELMRHSLOEYL-QNDTGSKI---- 326  
QY 73 HMLTQKI--AYQIASGLAYLHKNTIFCDLKSNDILVMSLDVKEHINIKLSDYISR--- 127  
DB 327 -HITQVDMAAQVAGSMAYLESRNTHRDLAARNVL-----VGEHNTYKADPGLAVFK 380  
QY 128 -----OSFHEGALGVETGPGYQAPRIRPIVDEKVMESYGMVLYELLS--GORPALG 179  
DB 381 VNEDIYESRHEIKLPVKWT---APEAIRSNKFSIKSDVMSFGILLYEITTYGKMEYSG 436  
QY 180 HHQDIAKLKSIGIRPVLGQPEEVQFRRLQALMECMTPEKRPALSVSQMKDPTFA 239  
DB 437 MTGAQVITQMLAQNYR--LPQSNCP-QQFYNTIMECWNAEPKER-----PTFE 481  
QY 240 TFWYEL 245  
DB 482 TLRWKL 487

RESULT 5  
US-08-492-723-2  
Sequence 2, Application US/08492723  
Patent No. 6531296  
GENERAL INFORMATION:  
APPLICANT: Lee, Edison T.  
APPLICANT: Craven, Rolf J.  
TITLE OF INVENTION: NUCLEAR TYROSINE KINASE RAK  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Selzer, Park & Gibson  
STREET: PO Box 34009  
CITY: Charlotte  
STATE: NO. 6531296th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/492,723  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:

NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5470-121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 505 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-492-723-2

Query Match  
Best Local Similarity 30.5%; Pred. No. 1.7e-14;  
Matches 75; Conservative 49; Mismatches 77; Indels 45; Gaps 11;

QY 15 SEPRQASMLHALQHPCTVALIGISI--HPLCFALSLAPLSLNTVLSENARDSSFTPLG 72  
DB 272 NDFLEAQIMKRLRHKTLQLYAVCTLEDPYITTELMRHSLOEYL-QNDTGSKI---- 326  
QY 73 HMLTQKI--AYQIASGLAYLHKNTIFCDLKSNDILVMSLDVKEHINIKLSDYISR--- 127  
DB 327 -HITQVDMAAQVAGSMAYLESRNTHRDLAARNVL-----VGEHNTYKADPGLAVFK 380  
QY 128 -----OSFHEGALGVETGPGYQAPRIRPIVDEKVMESYGMVLYELLS--GORPALG 179  
DB 381 VNEDIYESRHEIKLPVKWT---APEAIRSNKFSIKSDVMSFGILLYEITTYGKMEYSG 436  
QY 180 HHQDIAKLKSIGIRPVLGQPEEVQFRRLQALMECMTPEKRPALSVSQMKDPTFA 239  
DB 437 MTGAQVITQMLAQNYR--LPQSNCP-QQFYNTIMECWNAEPKER-----PTFE 481  
QY 240 TFWYEL 245  
DB 482 TLRWKL 487

RESULT 6  
PCT-US95-04228-20  
Sequence 20, Application PC/TUS9504228  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Bennett, Brian D.  
APPLICANT: Goeddel, David  
APPLICANT: Lee, James M.  
APPLICANT: Matthews, William  
APPLICANT: Teal, Siao Ping  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04228  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/222616  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 821P3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 505 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US95-04228-20

Query Match 6.4%; Score 243.5; DB 5; Length 505;  
Best Local Similarity 27.9%; Pred. No. 1.5e-14;  
Matches 75; Conservative 49; Mismatches 77; Indels 45; Gaps 11;

QY 15 SEFRQASMLHALQHPCTVALIGISIT--HPLCFALSLAPLSLNTVISENARDSSFIPLG 72  
DB 272 NDLFRAQIMKRLRHFKLQLYAVCTLEDPIYITELNRHSLQEYL-QNDTGSKI----- 326  
QY 73 HMLTCKI--AYQASLAVLHKNNIIFCDLSKNILVMSLDVKEHINKLSDDYISR--- 127  
DB 327 -HLLQGVDAQVQASMAWLESBNYIHRDLAARNV-----VGEHNTYKVADPELAEVFK 380  
QY 128 -----QSFEHGAALGVEGTPEGYOPEIRPRIVYDEKVMFSYGMVLYELLS--GQRPALG 179  
DB 381 VDNEDIYERHEIKLFPKWT---APEAIRSNKFSIKSDVMSFGILYEITTYKMPYSG 436  
QY 180 HHQLQIAKLSKIRPVLCQPEEVOFRRLQALMMECWDTKEKRPALSVSQMKDPTFA 239  
DB 437 MTGAQVYQMLAQNYR--LPQPSNCP-QCFYNIMLECMNAEKER-----PTFE 481  
QY 240 TFWYEL 245  
DB 482 TLEWKL 487

RESULT 7  
US-09-221-235-5  
Sequence 5, Application US/09221235  
Patent No. 6043040  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAPE-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: NMI-050  
CURRENT APPLICATION NUMBER: US/09/221,235  
CURRENT FILING DATE: 1998-12-28  
EARLIER APPLICATION NUMBER: 09/163,115  
EARLIER FILING DATE:  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-221-235-5

Query Match 6.4%; Score 243; DB 3; Length 455;  
Best Local Similarity 27.9%; Pred. No. 1.5e-14;  
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

QY 10 AMKNSEFRQASMLHALQHPCTVALIGISIMPLCFAL--ELAPLSLNTVISENARDSS 67  
DB 43 AVKGLKIKKEAEILSVLSHRNIIQFYGVILEPKNYGVITEVASIGSLYDINSNR--SE 100  
QY 68 FIPLGMLTQKIAVOIASGLAYLHK--NIIFCDLSKNILVMSLDVKEHINKLSDDY 124  
DB 101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKYIHRDLKSRNVVIAADGV-----LKICDFG 153  
QY 125 ISRQSFHGAALGVEGTPEGYOPEIRPRIVYDEKVMFSYGMVLYELLSGQRPALGHQ 184  
DB 154 ASRFHNTTMSLVGTPEPMAPBEVIOSLPVSETCTYISGVVLMMLTREVFPFGLEG 213

QY 185 IAKLSKIRPVLCQPEEVOF-----RRLQALMMECWDTKEKRPALSVSQMKDPTFA 239  
DB 214 VAWL-----VVEKNERLITPSSCPRSPFALLHQCEADAKRPSFKQIISLESMSND 266  
QY 240 TFWYELC 246  
DB 267 TSLPDKC 273

RESULT 8  
US-09-221-928-5  
Sequence 5, Application US/09221928  
Patent No. 6121030  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAPE-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: NMI-050  
CURRENT APPLICATION NUMBER: US/09/221,928  
CURRENT FILING DATE: 1998-12-28  
EARLIER APPLICATION NUMBER: 09/163,115  
EARLIER FILING DATE:  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-221-928-5

Query Match 6.4%; Score 243; DB 3; Length 455;  
Best Local Similarity 27.9%; Pred. No. 1.5e-14;  
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

QY 10 AMKNSEFRQASMLHALQHPCTVALIGISIMPLCFAL--ELAPLSLNTVISENARDSS 67  
DB 43 AVKGLKIKKEAEILSVLSHRNIIQFYGVILEPKNYGVITEVASIGSLYDINSNR--SE 100  
QY 68 FIPLGMLTQKIAVOIASGLAYLHK--NIIFCDLSKNILVMSLDVKEHINKLSDDY 124  
DB 101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKYIHRDLKSRNVVIAADGV-----LKICDFG 153  
QY 125 ISRQSFHGAALGVEGTPEGYOPEIRPRIVYDEKVMFSYGMVLYELLSGQRPALGHQ 184  
DB 154 ASRFHNTTMSLVGTPEPMAPBEVIOSLPVSETCTYISGVVLMMLTREVFPFGLEG 213  
QY 185 IAKLSKIRPVLCQPEEVOF-----RRLQALMMECWDTKEKRPALSVSQMKDPTFA 239  
DB 214 VAWL-----VVEKNERLITPSSCPRSPFALLHQCEADAKRPSFKQIISLESMSND 266  
QY 240 TFWYELC 246  
DB 267 TSLPDKC 273

RESULT 9  
US-09-221-527-5  
Sequence 5, Application US/09221527  
Patent No. 616832  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAPE-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: NMI-050  
CURRENT APPLICATION NUMBER: US/09/221,527  
CURRENT FILING DATE: 1998-12-28  
EARLIER APPLICATION NUMBER: 09/163,115  
EARLIER FILING DATE:  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-221-527-5

Query Match 6.4%; Score 243; DB 3; Length 455;

Best Local Similarity 27.9%; Pred. No. 1.5e-14;

Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

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QY 10 AMKNFSEFRQASMLHALQHPCTVALIGISIHPLCFAL--ELAPLSLNTVLSNARDSS 67
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Db 43 AVKLLKIKKEAEILSVLSHRNIIQFYGVILEPPRYGIVTEVASLSGLVDYINSNR--SE 100
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QY 68 FIPLGMLTQKIAVOIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124
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Db 101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVIAADGV----LKICDFG 153
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 125 ISROSFHEGALGVEGTGPGYOAPRIIVYDEKVMESYGMVLYELLSGORPALGHHQLQ 184
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 154 ASRFNNHTTHMSLVGTFPMMAPEVIGSLPVSETCDTYSYGVLMEMLTREVPEKGLGQLQ 213
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 185 IAKLSKGIKIRPVLGQPEEVQF-----RRLQALMMECDTKEKRPALSVSQMKDPTFA 239
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 214 VAWL-----VVEKNERLTIIPSCPRFAELHQCWEADAKKRPFRKQIISLESMSND 266
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 240 TFWYELC 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 267 TSLPDKC 273
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RESULT 10

US-09-221-236-5

Sequence 5, Application US/09221236

Patent No. 6146841

GENERAL INFORMATION:

APPLICANT: Acton, Susan

TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

FILE REFERENCE: NMT-050

CURRENT APPLICATION NUMBER: US/09/221,236

CURRENT FILING DATE: 1998-12-28

EARLIER APPLICATION NUMBER: 09/163,115

EARLIER FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-221-236-5

Query Match 6.4%; Score 243; DB 3; Length 455;

Best Local Similarity 27.9%; Pred. No. 1.5e-14;

Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

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QY 10 AMKNFSEFRQASMLHALQHPCTVALIGISIHPLCFAL--ELAPLSLNTVLSNARDSS 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 43 AVKLLKIKKEAEILSVLSHRNIIQFYGVILEPPRYGIVTEVASLSGLVDYINSNR--SE 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 FIPLGMLTQKIAVOIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVIAADGV----LKICDFG 153
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 125 ISROSFHEGALGVEGTGPGYOAPRIIVYDEKVMESYGMVLYELLSGORPALGHHQLQ 184
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Db 154 ASRFNNHTTHMSLVGTFPMMAPEVIGSLPVSETCDTYSYGVLMEMLTREVPEKGLGQLQ 213
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 185 IAKLSKGIKIRPVLGQPEEVQF-----RRLQALMMECDTKEKRPALSVSQMKDPTFA 239
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Db 214 VAWL-----VVEKNERLTIIPSCPRFAELHQCWEADAKKRPFRKQIISLESMSND 266
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QY 240 TFWYELC 246
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Db 267 TSLPDKC 273
```

RESULT 11

US-09-221-416-5

Sequence 5, Application US/09221416

Patent No. 6153417

GENERAL INFORMATION:

APPLICANT: Acton, Susan

TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

FILE REFERENCE: NMT-050

CURRENT APPLICATION NUMBER: US/09/221,416

CURRENT FILING DATE: 1998-12-28

EARLIER APPLICATION NUMBER: 09/163,115

EARLIER FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-221-416-5

Query Match 6.4%; Score 243; DB 3; Length 455;

Best Local Similarity 27.9%; Pred. No. 1.5e-14;

Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

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QY 10 AMKNFSEFRQASMLHALQHPCTVALIGISIHPLCFAL--ELAPLSLNTVLSNARDSS 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 43 AVKLLKIKKEAEILSVLSHRNIIQFYGVILEPPRYGIVTEVASLSGLVDYINSNR--SE 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 FIPLGMLTQKIAVOIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVIAADGV----LKICDFG 153
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 125 ISROSFHEGALGVEGTGPGYOAPRIIVYDEKVMESYGMVLYELLSGORPALGHHQLQ 184
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Db 154 ASRFNNHTTHMSLVGTFPMMAPEVIGSLPVSETCDTYSYGVLMEMLTREVPEKGLGQLQ 213
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 185 IAKLSKGIKIRPVLGQPEEVQF-----RRLQALMMECDTKEKRPALSVSQMKDPTFA 239
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 214 VAWL-----VVEKNERLTIIPSCPRFAELHQCWEADAKKRPFRKQIISLESMSND 266
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 240 TFWYELC 246
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Db 267 TSLPDKC 273
```

RESULT 12

US-09-221-245-5

Sequence 5, Application US/09221245

Patent No. 6180358

GENERAL INFORMATION:

APPLICANT: Acton, Susan

TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

FILE REFERENCE: NMT-050

CURRENT APPLICATION NUMBER: US/09/221,245

CURRENT FILING DATE: 1998-12-28

EARLIER APPLICATION NUMBER: US 09/163,115

EARLIER FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-221-245-5

Query Match 6.4%; Score 243; DB 3; Length 455;

Best Local Similarity 27.9%; Pred. No. 1.5e-14;

Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

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QY 10 AMKNFSEFRQASMLHALQHPCTVALIGISIHPLCFAL--ELAPLSLNTVLSNARDSS 67
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Db 43 AVKLLKIKKEAEILSVLSHRNIIQFYGVILEPPRYGIVTEVASLSGLVDYINSNR--SE 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 FIPLGMLTQKIAVOIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124
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Db 101 EMDMDHMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVVIAADGV-----LKTCDPG 153  
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Db 154 ASRFNHTTHMSLVGTFFPMWAPDEVIGSLPVSETCDTYSYGVLWEMLTREVPFKGLEGLQ 213  
QY 185 IAKKLSKGIKRPVILGQPEEVQF-----RRLOALMECNDTKREKRPALSVSQMKDPTFA 239  
Db 214 VAWL-----VVEKNERLTIPSSCPFSFAELLHQCEWADAKRPSFKQIISLESMSND 266  
QY 240 TFMVELC 246  
Db 267 TSLPDKC 273

RESULT 13  
US-09-163-115-5  
; Sequence 5, Application US/09163115A  
; Patent No. 6183962  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: NMI-050  
; CURRENT APPLICATION NUMBER: US/09/163,115A  
; CURRENT FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-163-115-5

Query Match 6.4%; Score 243; DB 3; Length 455;  
Best Local Similarity 27.9%; Pred. No. 1.5e-14;  
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;  
QY 10 AMKNFSEFROASMLHALQHPICIVALLIGISIHPLCPAL--ELAPLSLNTLVSENARDSS 67  
Db 43 AVKLLKTEKEAEILSVLSHRNIIQFYGVILLEPPNYGIVTEYASLSGLYDYNINR--SE 100  
QY 68 FIPLGMLTOKIAVQIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124  
Db 101 EMDMDHMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVVIAADGV-----LKTCDPG 153  
QY 125 ISROSFEHGALGVEGTPGYCAPEIRPRIYDEKVMFSYGMVLYELLSGORPALGHHOLQ 184  
Db 154 ASRFNHTTHMSLVGTFFPMWAPDEVIGSLPVSETCDTYSYGVLWEMLTREVPFKGLEGLQ 213  
QY 185 IAKKLSKGIKRPVILGQPEEVQF-----RRLOALMECNDTKREKRPALSVSQMKDPTFA 239  
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QY 240 TFMVELC 246  
Db 267 TSLPDKC 273

RESULT 14  
US-09-221-528-5  
; Sequence 5, Application US/09221528  
; Patent No. 6190874  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: NMI-050  
; CURRENT APPLICATION NUMBER: US/09/221,528  
; CURRENT FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; EARLIER FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-221-528-5

Query Match 6.4%; Score 243; DB 3; Length 455;  
Best Local Similarity 27.9%; Pred. No. 1.5e-14;  
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;  
QY 10 AMKNFSEFROASMLHALQHPICIVALLIGISIHPLCPAL--ELAPLSLNTLVSENARDSS 67  
Db 43 AVKLLKTEKEAEILSVLSHRNIIQFYGVILLEPPNYGIVTEYASLSGLYDYNINR--SE 100  
QY 68 FIPLGMLTOKIAVQIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124  
Db 101 EMDMDHMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVVIAADGV-----LKTCDPG 153  
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Db 154 ASRFNHTTHMSLVGTFFPMWAPDEVIGSLPVSETCDTYSYGVLWEMLTREVPFKGLEGLQ 213  
QY 185 IAKKLSKGIKRPVILGQPEEVQF-----RRLOALMECNDTKREKRPALSVSQMKDPTFA 239  
Db 214 VAWL-----VVEKNERLTIPSSCPFSFAELLHQCEWADAKRPSFKQIISLESMSND 266  
QY 240 TFMVELC 246  
Db 267 TSLPDKC 273

RESULT 15  
US-09-593-553-5  
; Sequence 5, Application US/09593553  
; Patent No. 6200770  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: NMI-050  
; CURRENT APPLICATION NUMBER: US/09/593,553  
; CURRENT FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: 09/163,115  
; PRIOR FILING DATE: 1998-09-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-593-553-5

Query Match 6.4%; Score 243; DB 3; Length 455;  
Best Local Similarity 27.9%; Pred. No. 1.5e-14;  
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;  
QY 10 AMKNFSEFROASMLHALQHPICIVALLIGISIHPLCPAL--ELAPLSLNTLVSENARDSS 67  
Db 43 AVKLLKTEKEAEILSVLSHRNIIQFYGVILLEPPNYGIVTEYASLSGLYDYNINR--SE 100  
QY 68 FIPLGMLTOKIAVQIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124  
Db 101 EMDMDHMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVVIAADGV-----LKTCDPG 153  
QY 125 ISROSFEHGALGVEGTPGYCAPEIRPRIYDEKVMFSYGMVLYELLSGORPALGHHOLQ 184  
Db 154 ASRFNHTTHMSLVGTFFPMWAPDEVIGSLPVSETCDTYSYGVLWEMLTREVPFKGLEGLQ 213  
QY 185 IAKKLSKGIKRPVILGQPEEVQF-----RRLOALMECNDTKREKRPALSVSQMKDPTFA 239  
Db 214 VAWL-----VVEKNERLTIPSSCPFSFAELLHQCEWADAKRPSFKQIISLESMSND 266  
QY 240 TFMVELC 246

Mon Dec 15 08:33:47 2003

us-09-836-392-21.rat

Page 7

Db 267 TSUPDKC 273

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Job time : 23 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 14, 2003, 07:15:16 ; Search time 36 Seconds

(without alignments)  
3761.003 Million cell updates/sec

Title: US-09-836-392-21

Perfect score: 3822  
Sequence: 1 MLRLRATDMKNFSEFROE.....IFYQSYELGLACTRKRR 728

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

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Post-Processing: Minimum Match 0%

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Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	3822	100.0	728	US-09-836-392-21	Sequence 21, Appl
2	3574.5	93.5	1987	US-10-132-382-6	Sequence 6, Appl
3	3574.5	93.5	2013	US-10-132-382-2	Sequence 2, Appl
4	3574.5	93.5	2014	US-10-132-382-8	Sequence 8, Appl
5	3574.5	93.5	2040	US-10-132-382-4	Sequence 4, Appl
6	2523	66.0	501	US-10-094-749-1689	Sequence 1689, Ap
7	335.5	8.5	911	US-10-115-482-48	Sequence 48, Appl
8	327.5	8.6	911	US-10-115-482-50	Sequence 50, Appl
9	327.5	8.6	1818	US-10-335-687A-2	Sequence 2, Appl
10	327.5	8.6	1824	US-10-335-687A-5	Sequence 5, Appl
11	275.5	7.2	394	US-09-862-027-19	Sequence 19, Appl
12	271	7.1	252	US-09-976-782-41	Sequence 41, Appl
13	271	7.1	254	US-09-976-782-30	Sequence 30, Appl
14	271	7.1	255	US-09-863-776-41	Sequence 41, Appl
15	267.5	7.0	1097	US-10-288-798-12	Sequence 12, Appl

15	263	6.9	1036	US-10-354-358-24	Sequence 24, Appl
17	263	6.9	1036	US-10-014-882-2	Sequence 2, Appl
18	260.5	6.8	847	US-10-143-133-2	Sequence 2, Appl
19	250.5	6.6	765	US-10-128-174-36	Sequence 36, Appl
20	247.5	6.5	765	US-10-128-174-3	Sequence 3, Appl
21	247.5	6.5	765	US-10-128-174-35	Sequence 35, Appl
22	247.5	6.5	765	US-10-128-174-44	Sequence 44, Appl
23	246.5	6.4	765	US-10-128-174-37	Sequence 37, Appl
24	246.5	6.4	765	US-10-128-174-39	Sequence 39, Appl
25	246.5	6.4	765	US-10-128-174-42	Sequence 42, Appl
26	246.5	6.4	823	US-10-128-174-43	Sequence 43, Appl
27	244.5	6.4	823	US-10-376-564-63	Sequence 63, Appl
28	244	6.4	257	US-09-863-776-42	Sequence 42, Appl
29	243.5	6.4	505	US-09-977-269-6	Sequence 6, Appl
30	243.5	6.4	505	US-09-882-610-20	Sequence 20, Appl
31	243.5	6.4	505	US-09-877-260-6	Sequence 6, Appl
32	243.5	6.4	505	US-09-877-261-6	Sequence 6, Appl
33	243	6.4	455	US-09-757-982-5	Sequence 5, Appl
34	243	6.4	455	US-10-094-749-2477	Sequence 2477, Ap
35	242.5	6.3	850	US-10-128-174-41	Sequence 41, Appl
36	242.5	6.3	850	US-09-823-189-2	Sequence 2, Appl
37	242	6.3	257	US-09-823-187-46	Sequence 46, Appl
38	241.5	6.3	765	US-10-128-174-38	Sequence 38, Appl
39	241.5	6.3	765	US-10-128-174-40	Sequence 40, Appl
40	240.5	6.3	349	US-10-106-698-6345	Sequence 6345, Ap
41	239.5	6.3	765	US-10-128-174-34	Sequence 34, Appl
42	238	6.2	937	US-09-974-298-129	Sequence 129, App
43	237	6.2	425	US-09-828-113-29	Sequence 29, Appl
44	236	6.2	263	US-09-840-704-5	Sequence 5, Appl
45	236	6.2	821	US-10-171-404A-48	Sequence 48, Appl

## ALIGNMENTS

RESULT 1  
US-09-836-392-21  
Sequence 21, Application US/09836392  
Patent No. US20020173458A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypept  
FILE REFERENCES: PTO2001  
CURRENT APPLICATION NUMBER: US/09/836,392  
CURRENT FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: PCT/US00/28066  
PRIOR FILING DATE: 2000-10-11  
PRIOR APPLICATION NUMBER: 60/159,542  
PRIOR FILING DATE: 1999-10-15  
PRIOR APPLICATION NUMBER: 60/165,914  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 60/189,027  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 21  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-836-392-21

Query Match  
Best Local Similarity 100.0%; Score 3822; DB 10; Length 728;  
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLRLRATDMKNFSEFROEASMLHLPICVIALGISIHPLCPALBAPISLNTVLS 60  
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DB 61 ENADSSFIFLGHMLTOKIAYQIASGLAYLHKNNITFCOLKSDNITWISLDVKEHINTL 120

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DB 121 SDYGISRQSFHEGALGVEGTGPGYQAPERIRIYDEKVMFSYGMVLYELLSSQRPALGH 180  
QY 181 HOLOIAKLSKIGIRPVLGQPEEVOFRRLQALMMECWDTKPEKRPALSLSVSOMQDPTFAT 240  
DB 181 HOLOIAKLSKIGIRPVLGQPEEVOFRRLQALMMECWDTKPEKRPALSLSVSOMQDPTFAT 240  
QY 241 FMYELCCGKQIAFFSSQGOEYTVFMWCKESERNYVNTNTEKLMVEVORMCPCGMVNSQ 300  
DB 241 FMYELCCGKQIAFFSSQGOEYTVFMWCKESERNYVNTNTEKLMVEVORMCPCGMVNSQ 300  
QY 301 LOVORSLMTATEOKIYITLKGMCPLNTPQALDTPAVVTCFLAVPIKNSYLVLAGL 360  
DB 301 LOVORSLMTATEOKIYITLKGMCPLNTPQALDTPAVVTCFLAVPIKNSYLVLAGL 360  
QY 361 ADGLVAVFPVVRGTPKDCSYLCSHTANRSKFSIADBDARQNPYPVKAMEVUNSGSEVMY 420  
DB 361 ADGLVAVFPVVRGTPKDCSYLCSHTANRSKFSIADBDARQNPYPVKAMEVUNSGSEVMY 420  
QY 421 SNPGSLVITDCASLEICRLEPYMAPSMVTSVYVCSSEGRGEVVMCLDDKXANSLVMYHST 480  
DB 421 SNPGSLVITDCASLEICRLEPYMAPSMVTSVYVCSSEGRGEVVMCLDDKXANSLVMYHST 480  
QY 481 TYOLCARYFCGVPSPRLDMFPVRPLDTEPPAASHNTANPKYBEDDSIADVSIMYSEELGTQ 540  
DB 481 TYOLCARYFCGVPSPRLDMFPVRPLDTEPPAASHNTANPKYBEDDSIADVSIMYSEELGTQ 540  
QY 541 ILIHQESLTDYCSMSYSSSPPROAARSBSLSPSSPASSSVFSTDCEDSDMLHTPGAA 600  
DB 541 ILIHQESLTDYCSMSYSSSPPROAARSBSLSPSSPASSSVFSTDCEDSDMLHTPGAA 600  
QY 601 SDRSEHDLTPMDGSETFSQHQAQVXILAVRDLIWPBRGGDVIYIGLEKDSQAQGRVIAV 660  
DB 601 SDRSEHDLTPMDGSETFSQHQAQVXILAVRDLIWPBRGGDVIYIGLEKDSQAQGRVIAV 660  
QY 661 LKARELTPHGVLVDAVAVAKOTVCTFENENTEMCLAVMRGMGAREFDIFYOSYELGRL 720  
DB 661 LKARELTPHGVLVDAVAVAKOTVCTFENENTEMCLAVMRGMGAREFDIFYOSYELGRL 720  
QY 721 EACTRKRR 728  
DB 721 EACTRKRR 728

RESULT 2  
US-10-132-382-6  
; Sequence 6, Application US/10132382  
; Publication No. US20030045699A1  
; GENERAL INFORMATION:  
; APPLICANT: WEISS, BERTRAM  
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS  
; FILE REFERENCE: SCH-1811  
; CURRENT APPLICATION NUMBER: US/10/132,382  
; CURRENT FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1987  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-132-382-6

Query Match 93.5%; Score 3574.5; DB 15; Length 1987;  
Best Local Similarity 94.5%; Pred. No. 4,4e-296;  
Matches 687; Conservative 0; Mismatches 1; Indels 39; Gaps 1;

QY 1 MRRHRLATDAMKNSSEFRQASMLHALQHPCTIVALLGISIHPLCFALSLAPLSLNTVLS 60

DB 1300 MRRHRLATDAMKNSSEFRQASMLHALQHPCTIVALLGISIHPLCFALSLAPLSLNTVLS 1359

QY 61 ENARDSSEFPLGHMLTQKIAVOIASGLAVLHKNNIIFCDLKSNDILVMSLDVKEHINIKL 120

DB 1360 ENARDSSEFPLGHMLTQKIAVOIASGLAVLHKNNIIFCDLKSNDILVMSLDVKEHINIKL 1419  
QY 121 SDYGISRQSFHEGALGVEGTGPGYQAPERIRIYDEKVMFSYGMVLYELLSSQRPALGH 180  
DB 1420 SDYGISRQSFHEGALGVEGTGPGYQAPERIRIYDEKVMFSYGMVLYELLSSQRPALGH 1479  
QY 181 HOLOIAKLSKIGIRPVLGQPEEVOFRRLQALMMECWDTKPEKRPALSLSVSOMQDPTFAT 240  
DB 181 HOLOIAKLSKIGIRPVLGQPEEVOFRRLQALMMECWDTKPEKRPALSLSVSOMQDPTFAT 240  
QY 241 FMYELCCGKQIAFFSSQGOEYTVFMWCKESERNYVNTNTEKLMVEVORMCPCGMVNSQ 300  
DB 241 FMYELCCGKQIAFFSSQGOEYTVFMWCKESERNYVNTNTEKLMVEVORMCPCGMVNSQ 300  
QY 301 LOVORSLMTATEOKIYITLKGMCPLNTPQALDTPAVVTCFLAVPIKNSYLVLAGL 360  
DB 301 LOVORSLMTATEOKIYITLKGMCPLNTPQALDTPAVVTCFLAVPIKNSYLVLAGL 360  
QY 361 ADGLVAVFPVVRGTPKDCSYLCSHTANRSKFSIADBDARQNPYPVKAMEVUNSGSEVMY 420  
DB 361 ADGLVAVFPVVRGTPKDCSYLCSHTANRSKFSIADBDARQNPYPVKAMEVUNSGSEVMY 420  
QY 421 SNPGSLVITDCASLEICRLEPYMAPSMVTSVYVCSSEGRGEVVMCLDDKXANSLVMYHST 480  
DB 421 SNPGSLVITDCASLEICRLEPYMAPSMVTSVYVCSSEGRGEVVMCLDDKXANSLVMYHST 480  
QY 481 TYOLCARYFCGVPSPRLDMFPVRPLDTEPPAASHNTANPKYBEDDSIADVSIMYSEELGTQ 540  
DB 481 TYOLCARYFCGVPSPRLDMFPVRPLDTEPPAASHNTANPKYBEDDSIADVSIMYSEELGTQ 540  
QY 541 ILIHQESLTDYCSMSYSSSPPROAARSBSLSPSSPASSSVFSTDCEDSDMLHTPGAA 600  
DB 541 ILIHQESLTDYCSMSYSSSPPROAARSBSLSPSSPASSSVFSTDCEDSDMLHTPGAA 600  
QY 601 SDRSEHDLTPMDGSETFSQHQAQVXILAVRDLIWPBRGGDVIYIGLEKDSQAQGRVIAV 660  
DB 601 SDRSEHDLTPMDGSETFSQHQAQVXILAVRDLIWPBRGGDVIYIGLEKDSQAQGRVIAV 660  
QY 661 LKARELTPHGVLVDAVAVAKOTVCTFENENTEMCLAVMRGMGAREFDIFYOSYELGRL 720  
DB 661 LKARELTPHGVLVDAVAVAKOTVCTFENENTEMCLAVMRGMGAREFDIFYOSYELGRL 720  
QY 721 EACTRKRR 727  
DB 721 EACTRKRR 727

RESULT 3  
US-10-132-382-2  
; Sequence 2, Application US/10132382  
; Publication No. US20030045699A1  
; GENERAL INFORMATION:  
; APPLICANT: WEISS, BERTRAM  
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS  
; FILE REFERENCE: SCH-1811  
; CURRENT APPLICATION NUMBER: US/10/132,382  
; CURRENT FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2013  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-132-382-2

Query Match 93.5%; Score 3574.5; DB 15; Length 2013;  
Best Local Similarity 94.5%; Pred. No. 4,5e-296;  
Matches 687; Conservative 0; Mismatches 1; Indels 39; Gaps 1;

QY 1 MRRHRLATDAMKNSSEFRQASMLHALQHPCTIVALLGISIHPLCFALSLAPLSLNTVLS 60

DB 1326 MRRHRLATDAMKNSSEFRQASMLHALQHPCTIVALLGISIHPLCFALSLAPLSLNTVLS 1385

QY 61 ENARDSSFIPLGHMLTOKIAYQIASGLAYLHKNNIIFCDLKSNDILWMSLDVKEHINIKL 120  
 DB 1386 ENARDSSFIPLGHMLTOKIAYQIASGLAYLHKNNIIFCDLKSNDILWMSLDVKEHINIKL 1445  
 QY 121 SDYGISRQSFHEGALGVEGTGQYQAPRIPIVYDEKDMFSYGMVLYELLSGORPALGH 180  
 DB 1446 SDYGISRQSFHEGALGVEGTGQYQAPRIPIVYDEKDMFSYGMVLYELLSGORPALGH 1505  
 QY 181 HOLOIAKLKSKIRPVLOGPEEVQFRLOALMECMTDPEKRPALASVVSQMDPTPAT 240  
 DB 1506 HOLOIAKLKSKIRPVLOGPEEVQFRLOALMECMTDPEKRPALASVVSQMDPTPAT 1565  
 QY 241 FMYELCCGKOTAFSSQGOEYTVVFMWDEKESRNYTVNTEKIMEVQRMCCPGMKVSCQ 300  
 DB 1566 FMYELCCGKOTAFSSQGOEYTVVFMWDEKESRNYTVNTEKIMEVQRMCCPGMKVSCQ 1625  
 QY 301 LOVQSLMTATEDQKIYITLKGMCPLNTPOALDTPAVVTCFLAVPIKKNSYLVLAGL 360  
 DB 1626 LOVQSLMTATEDQKIYITLKGMCPLNTPOALDTPAVVTCFLAVPIKKNSYLVLAGL 1646  
 QY 361 ADGLVAVFPVVRGTGPKDSCSYLCGHTANRKSFIADBDARQNPYPVYKAMEVYVNSGSEVWY 420  
 DB 1647 ADGLVAVFPVVRGTGPKDSCSYLCGHTANRKSFIADBDARQNPYPVYKAMEVYVNSGSEVWY 1706  
 QY 421 SNGPGLLVIDCASLEICRLEPYPMAPSMVTSVVCSSEGRGEVWVCLDDKANSIWMYHST 480  
 DB 1707 SNGPGLLVIDCASLEICRLEPYPMAPSMVTSVVCSSEGRGEVWVCLDDKANSIWMYHST 1766  
 QY 481 TYQLCARFYCGVPSPLRDMFPVRPLDTEPPAASHANPKVPEGDSIADVSIYSEELGTQ 540  
 DB 1767 TYQLCARFYCGVPSPLRDMFPVRPLDTEPPAASHANPKVPEGDSIADVSIYSEELGTQ 1826  
 QY 541 ILIHQESLTDYCSMSYSSPPROAARSPSLPSSPASSSVFSTDCEDSDMLHTPGAA 600  
 DB 1827 ILIHQESLTDYCSMSYSSPPROAARSPSLPSSPASSSVFSTDCEDSDMLHTPGAA 1886  
 QY 601 SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWPBRGGDVIVIGLEKDSAGRGYIAV 660  
 DB 1887 SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWPBRGGDVIVIGLEKDSAGRGYIAV 1946  
 QY 661 LKARELTPHGVLDVAVAVKDVTVCTEFENENTEWCLAVRWGAGAREFDIFYQSYEELGRL 720  
 DB 1947 LKARELTPHGVLDVAVAVKDVTVCTEFENENTEWCLAVRWGAGAREFDIFYQSYEELGRL 2006  
 QY 721 EACTRKR 727  
 DB 2007 EACTRKR 2013

RESULT 4  
 US-10-132-382-8  
 ; Sequence 8, Application US/10132382  
 ; Publication No. US20030045699A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEISS, BERTRAM  
 ; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS  
 ; FILE REFERENCE: SCH-1811  
 ; CURRENT APPLICATION NUMBER: US/10/132.382  
 ; CURRENT FILING DATE: 2002-04-26  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 2014  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-132-382-8

Query Match 93.5%; Score 3574.5; DB 15; Length 2014;  
 Best Local Similarity 94.5%; Pred. No. 4.5e-296;  
 Matches 687; Conservative 0; Mismatches 1; Indels 39; Gaps 1;  
 QY 1 MURHRAIDAMKNFSEFRQASMLHALQHPICIVALLIGISIHPLCFALFALAPLSLNTVLVS 60

DB 1327 MURHRAIDAMKNFSEFRQASMLHALQHPICIVALLIGISIHPLCFALFALAPLSLNTVLVS 1386  
 QY 61 ENARDSSFIPLGHMLTOKIAYQIASGLAYLHKNNIIFCDLKSNDILWMSLDVKEHINIKL 120  
 DB 1387 ENARDSSFIPLGHMLTOKIAYQIASGLAYLHKNNIIFCDLKSNDILWMSLDVKEHINIKL 1446  
 QY 121 SDYGISRQSFHEGALGVEGTGQYQAPRIPIVYDEKDMFSYGMVLYELLSGORPALGH 180  
 DB 1447 SDYGISRQSFHEGALGVEGTGQYQAPRIPIVYDEKDMFSYGMVLYELLSGORPALGH 1506  
 QY 181 HOLOIAKLKSKIRPVLOGPEEVQFRLOALMECMTDPEKRPALASVVSQMDPTPAT 240  
 DB 1507 HOLOIAKLKSKIRPVLOGPEEVQFRLOALMECMTDPEKRPALASVVSQMDPTPAT 1566  
 QY 241 FMYELCCGKOTAFSSQGOEYTVVFMWDEKESRNYTVNTEKIMEVQRMCCPGMKVSCQ 300  
 DB 1567 FMYELCCGKOTAFSSQGOEYTVVFMWDEKESRNYTVNTEKIMEVQRMCCPGMKVSCQ 1626  
 QY 301 LOVQSLMTATEDQKIYITLKGMCPLNTPOALDTPAVVTCFLAVPIKKNSYLVLAGL 360  
 DB 1627 LOVQSLMTATEDQKIYITLKGMCPLNTPOALDTPAVVTCFLAVPIKKNSYLVLAGL 1647  
 QY 361 ADGLVAVFPVVRGTGPKDSCSYLCGHTANRKSFIADBDARQNPYPVYKAMEVYVNSGSEVWY 420  
 DB 1648 ADGLVAVFPVVRGTGPKDSCSYLCGHTANRKSFIADBDARQNPYPVYKAMEVYVNSGSEVWY 1707  
 QY 421 SNGPGLLVIDCASLEICRLEPYPMAPSMVTSVVCSSEGRGEVWVCLDDKANSIWMYHST 480  
 DB 1708 SNGPGLLVIDCASLEICRLEPYPMAPSMVTSVVCSSEGRGEVWVCLDDKANSIWMYHST 1767  
 QY 481 TYQLCARFYCGVPSPLRDMFPVRPLDTEPPAASHANPKVPEGDSIADVSIYSEELGTQ 540  
 DB 1768 TYQLCARFYCGVPSPLRDMFPVRPLDTEPPAASHANPKVPEGDSIADVSIYSEELGTQ 1827  
 QY 541 ILIHQESLTDYCSMSYSSPPROAARSPSLPSSPASSSVFSTDCEDSDMLHTPGAA 600  
 DB 1828 ILIHQESLTDYCSMSYSSPPROAARSPSLPSSPASSSVFSTDCEDSDMLHTPGAA 1887  
 QY 601 SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWPBRGGDVIVIGLEKDSAGRGYIAV 660  
 DB 1888 SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWPBRGGDVIVIGLEKDSAGRGYIAV 1947  
 QY 661 LKARELTPHGVLDVAVAVKDVTVCTEFENENTEWCLAVRWGAGAREFDIFYQSYEELGRL 720  
 DB 1948 LKARELTPHGVLDVAVAVKDVTVCTEFENENTEWCLAVRWGAGAREFDIFYQSYEELGRL 2007  
 QY 721 EACTRKR 727  
 DB 2008 EACTRKR 2014

RESULT 5  
 US-10-132-382-4  
 ; Sequence 4, Application US/10132382  
 ; Publication No. US20030045699A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEISS, BERTRAM  
 ; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS  
 ; FILE REFERENCE: SCH-1811  
 ; CURRENT APPLICATION NUMBER: US/10/132.382  
 ; CURRENT FILING DATE: 2002-04-26  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 2040  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-132-382-4

Query Match 93.5%; Score 3574.5; DB 15; Length 2040;  
 Best Local Similarity 94.5%; Pred. No. 4.6e-296;  
 Matches 687; Conservative 0; Mismatches 1; Indels 39; Gaps 1;

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QY      1 MNRHRLATDAMKNSFSEFROEASMLHALQHPICVIALIGISIHPLCPALBLAELASLNTVLS 60
DB      1353 MNRHRLATDAMKNSFSEFROEASMLHALQHPICVIALIGISIHPLCPALBLAELASLNTVLS 1412
QY      61 ENARDSSTPLGLMLOKTAAYQIASGLATLHKNNITFCDLSDNILVMSLWKEHINIKL 120
DB      1413 ENARDSSTPLGLMLOKTAAYQIASGLATLHKNNITFCDLSDNILVMSLWKEHINIKL 1472
QY      121 SDYGISROSFEHAGLVEGTGVOAPEIRPIVYDEKVMESYGVMTYELLSGORPALGH 180
DB      1473 SDYGISROSFEHAGLVEGTGVOAPEIRPIVYDEKVMESYGVMTYELLSGORPALGH 1532
QY      181 HOLOIAKUSKSGIRPVYLGQPEEYQFRRLQALMECWDTPKPRPLATLSVSOQMDPTFAT 240
DB      1533 HOLOIAKUSKSGIRPVYLGQPEEYQFRRLQALMECWDTPKPRPLATLSVSOQMDPTFAT 1592
QY      241 FMYELCCGKOTAFSSQOGGYTVFWDGKEESRNTYVNTKGLMEVQRMCCPGMKYSQ 300
DB      1593 FMYELCCGKOTAFSSQOGGYTVFWDGKEESRNTYVNTKGLMEVQRMCCPGMKYSQ 1652
QY      301 LOYORSIMWTATEDOKIYITLKMCPINTPOALDTPAVVTCFLAVPIKKNSTYVLAGL 360
DB      1653 LOYORSIMWTATEDOKIYITLKMCPINTPOALDTPAVVTCFLAVPIKKNSTYVLAGL 1673
QY      361 ADGLVAVFPVYRGTPKDSGSCSYLCSHTANKSKFSIADBDARONPYPYKAMEVYNSGSEVWY 420
DB      1674 ADGLVAVFPVYRGTPKDSGSCSYLCSHTANKSKFSIADBDARONPYPYKAMEVYNSGSEVWY 1733
QY      421 SNGPGLLVIDCASLEICRLEPYMAESMTSVYCSSEGRSEVWCLDDKANSIWMYHST 480
DB      1734 SNGPGLLVIDCASLEICRLEPYMAESMTSVYCSSEGRSEVWCLDDKANSIWMYHST 1793
QY      481 TYOLCARFCGVSPRLDMFPVRLDTEPPASHANPVPBGDSIAVSIWYSEBELGTQ 540
DB      1794 TYOLCARFCGVSPRLDMFPVRLDTEPPASHANPVPBGDSIAVSIWYSEBELGTQ 1853
QY      541 ILIHOSLTDYCSMSSYSSSPROARSPSLPSSPASSSVPSFTDCEDESDMLHTPPAA 600
DB      1854 ILIHOSLTDYCSMSSYSSSPROARSPSLPSSPASSSVPSFTDCEDESDMLHTPPAA 1913
QY      601 SDRSEHDLTMDDETSSQHLQAVKIILAVRDLIWPRRGDVIYVLEKDSORAGRYAV 660
DB      1914 SDRSEHDLTMDDETSSQHLQAVKIILAVRDLIWPRRGDVIYVLEKDSORAGRYAV 1973
QY      661 LKARELTPHGVLDAAVVAADTVCTFENENTEMCLAVWRGGALEFDIFQSYEELGRL 720
DB      1974 LKARELTPHGVLDAAVVAADTVCTFENENTEMCLAVWRGGALEFDIFQSYEELGRL 2033
QY      721 EACTRKA 727
DB      2034 EACTRKA 2040

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RESULT 6  
US-10-094-749-1689  
Sequence 1689, Application US/10094749  
Publication No. US20030219741A1  
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHICO

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APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1689
TYPE: PR
ORGANISM: Homo sapiens
US-10-094-749-1689

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Query Match 66.0% Score 2523; DB 12; Length 501;  
Best Local Similarity 100.0%; Prid. No. 5e-207;  
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      160 MFSYGMVLYELSGORPALGHQIARKLSKGRIPVYLGQPEEYQFRRLQALMECWDTK 219
DB      1 MFSYGMVLYELSGORPALGHQIARKLSKGRIPVYLGQPEEYQFRRLQALMECWDTK 60
QY      220 PEKRPALASVVSQMDPTFATFMYELCCGKOTAFSSQOGGYTVFWDGKEESRNTYV 279
DB      61 PEKRPALASVVSQMDPTFATFMYELCCGKOTAFSSQOGGYTVFWDGKEESRNTYV 120
QY      280 TEKGLMEVQRMCCPGMKYSQLOYORSIMWTATEDOKIYITLKMCPINTPOALDTPAV 339
DB      121 TEKGLMEVQRMCCPGMKYSQLOYORSIMWTATEDOKIYITLKMCPINTPOALDTPAV 180
QY      340 VTCFLAVPIKKNSTYVLAGLADGLVAVFPVYRGTPKDSGSCSYLCSHTANKSKFSIADEDA 399
DB      181 VTCFLAVPIKKNSTYVLAGLADGLVAVFPVYRGTPKDSGSCSYLCSHTANKSKFSIADEDA 240
QY      400 ROPYPYKAMEVYNSGSEVWYNSNGPGLLVIDCASLEICRLEPYMAESMTSVYCSSEGR 459
DB      241 ROPYPYKAMEVYNSGSEVWYNSNGPGLLVIDCASLEICRLEPYMAESMTSVYCSSEGR 300
QY      460 GEEVWVCLDDKANSIWMYHSTTYOLCARFCGVSPRLDMFPVRLDTEPPASHANPK 519
DB      301 GEEVWVCLDDKANSIWMYHSTTYOLCARFCGVSPRLDMFPVRLDTEPPASHANPK 360
QY      520 VREGDSIADVSIWYSEBELGTQILIHOSLTDYCSMSSYSSPPROARSPSLPSSPASS 579
DB      361 VREGDSIADVSIWYSEBELGTQILIHOSLTDYCSMSSYSSPPROARSPSLPSSPASS 420
QY      580 SSVPFSTDCEDSDMLHTPGAASDRSEHDLTMDDETSSQHLQAVKIILAVRDLIWPRR 637
DB      421 SSVPFSTDCEDSDMLHTPGAASDRSEHDLTMDDETSSQHLQAVKIILAVRDLIWPRR 478

```

RESULT 7  
US-10-115-482-48  
Sequence 48, Application US/10115482  
Publication No. US20030212257A1  
GENERAL INFORMATION:

APPLICANT: Spvtek, et al.  
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM  
TITLE OF INVENTION: AND METHODS  
FILE REFERENCE: 21404-322D  
CURRENT APPLICATION NUMBER: US/10/115,482  
CURRENT FILING DATE: 2002-04-05  
PRIOR APPLICATION NUMBER: 60/281,086  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03

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/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,512
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ PRIOR APPLICATION NUMBER: 60/285,890
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: 60/286,068
/ PRIOR FILING DATE: 2001-04-24
/ PRIOR APPLICATION NUMBER: 60/286,292
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: 60/287,213
/ PRIOR FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: 60/288,257
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/291,134
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 60/282,020
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/291,725
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/294,771
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: 60/296,965
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: 60/299,128
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 149
/ SEQ ID NO 48
/ LENGTH: 915
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-115-482-48

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Query Match      8.8%; Score 335.5; DB 12; Length 915;
Best Local Similarity 26.9%; Pred. No. 1.6e-19;
Matches 106; Conservative 76; Mismatches 159; Indels 53; Gaps 14;

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QY 10 AMKNFSE-----FROEASMLHALOHPCTVALIGISIHPLCFALSLAPLSINTVLSENA 63
DB 238 AVKIFNKHTSLRLRQELVVLCHLHPSLISLAAGIRPRMLVMEASKSGSLDRLLQDQK 357
QY 64 RDSFIFLGHMLTOKIAVOASGLAVLHKNNIFCDLKSNNILVMSLDVKEHINIKLSY 123
DB 358 AS-----LRTLIQHRILAHVADGLRYLHSAAMIYRDLKPHNVLLFTLYPNAALITAKIADY 412
QY 124 GISROSFHEGALGVGTPGYQAPRI-RPRIYDEKVMFSYGMVLYELL-SGORPALG-- 179
DB 413 GIAOYCCRMGKITSGTGFRAPEVARGNVITNQAADVSGFLLYDILTTGGRITVEGLK 472
QY 180 ----HHOLOIAKLSKIGIRPVLGQPEEVOFRRLQALMECHMDTKEKRPALSVVSQMKD 235
DB 473 FPNFDELEIOGKLPDPVKEYGCAP-----WFWVEKLTKOCLKENPQERPTSQAVFQVDPD 528
QY 236 PTFATFMYELCCGKO-----TAFSSQOGEYTVFMDG-----KESSRYVTVNTE 281
DB 529 ILNSA---ELVCLTRRILLPRKNVIVECNVATHHNSRNASTNLGSGHTRDQQLSFLDLNTE 585
QY 282 KGLMEV---QRMCCGKAVSCQLOVQSLM--TATEDOKIYITLKGMCPLNTPQALDT 336
DB 586 GYTSEEVADSRILCAL--VHLPEKESWTVSGTQSGTLVINTDEGKKRHTLEKMTDS 642
QY 337 PAVTTCFLAVPIK--KNSYLVLAGIADGVAVF 368
DB 643 ---VTCLYCNSEFSKSKOKMFLVGTADGKLAIF 673

```

RESULT 8

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US-10-115-482-50
/ Sequence 50, Application US/10115482
/ Publication No. US20030212257A1
/ GENERAL INFORMATION:
/ APPLICANT: Spylek, et al.
/ TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
/ TITLE OF INVENTION: AND METHODS
/ FILE REFERENCE: 21404-322D
/ CURRENT FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/281,086
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,512
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ PRIOR APPLICATION NUMBER: 60/285,890
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: 60/286,068
/ PRIOR FILING DATE: 2001-04-24
/ PRIOR APPLICATION NUMBER: 60/286,292
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: 60/287,213
/ PRIOR FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: 60/288,257
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/291,134
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 60/282,020
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/291,725
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/294,771
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: 60/296,965
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: 60/299,128
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 149
/ SEQ ID NO 50
/ LENGTH: 911
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-115-482-50

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Query Match      8.6%; Score 327.5; DB 12; Length 911;
Best Local Similarity 26.1%; Pred. No. 7.9e-19;
Matches 101; Conservative 75; Mismatches 168; Indels 43; Gaps 13;

```

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QY 10 AMKNFSE-----FROEASMLHALOHPCTVALIGISIHPLCFALSLAPLSINTVLSENA 63
DB 238 AVKIFNKHTSLRLRQELVVLCHLHPSLISLAAGIRPRMLVMEASKSGSLDRLLQDQK 357
QY 64 RDSFIFLGHMLTOKIAVOASGLAVLHKNNIFCDLKSNNILVMSLDVKEHINIKLSY 123
DB 358 AS-----LRTLIQHRILAHVADGLRYLHSAAMIYRDLKPHNVLLFTLYPNAALITAKIADY 412
QY 124 GISROSFHEGALGVGTPGYQAPRI-RPRIYDEKVMFSYGMVLYELL-SGORPALG-- 179
DB 413 GIAOYCCRMGKITSGTGFRAPEVARGNVITNQAADVSGFLLYDILTTGGRITVEGLK 472
QY 180 ----HHOLOIAKLSKIGIRPVLGQPEEVOFRRLQALMECHMDTKEKRPALSVVSQMKD 235
DB 473 FPNFDELEIOGKLPDPVKEYGCAP-----WFWVEKLTKOCLKENPQERPTSQAVFQVDPD 528

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RESULT 10  
US-10-335-687A-5  
; Sequence 5, Application US/10335687A  
; Publication No. US20030166222A1

Query Match	7.28;	Score 275.5;	DB 10;	Length 394
Best Local Similarity	31.38;	Pred. No. 6.3e-15;		



QY 177 ALGHQLOIAKLSKGRVLPQ-----EVQFRRIQALMECWDTKRKPPLASV 230  
DB 199 FPGIDPLELFRKE--RPRRLPLPPNCSE-----LKDIKKCINKDPKRPFAKEIL 251  
QY 231 S 231  
DB 252 N 252

## RESULT 14

US-09-863-776-41  
Sequence 41, Application US/09863776  
Publication No. US20030198953A1  
GENERAL INFORMATION:  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Majumder, Kumud  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Mishra, Vishnu  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Spaderu, Steven K  
APPLICANT: Shenoy, Suresh G  
APPLICANT: Rastelli, Luca  
APPLICANT: Li, Li  
APPLICANT: Taupier, Raymond J  
APPLICANT: Gangolli, Bsha  
TITLE OF INVENTION: No. US20030198953A1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-020  
CURRENT APPLICATION NUMBER: US/09/863,776  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: 09/540,763  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: 60/206,679  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 60/206,688  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 60/206,829  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 60/207,748  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: 60/207,798  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: 60/208,263  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 60/208,831  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: 60/209,451  
PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: 60/210,060  
PRIOR FILING DATE: 2000-06-07  
PRIOR APPLICATION NUMBER: 60/219,507  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: 60/221,337  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/221,927  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: 60/263,135  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,698  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/263,694  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 256  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Protein Kinase

US-09-863-776-41  
OTHER INFORMATION: domain Consensus Sequence

Query Match 7.1%; Score 271; DB 12; Length 256;

Best Local Similarity 32.4%; Pred. No. 8,1e-15;  
Matches 78; Conservative 42; Mismatches 93; Indels 28; Gaps 7;  
QY 2 LHLELATAMKNFESEFOASMLALOPICVALIGI--SIHPLCFALBAPUSINTVL 59  
DB 29 IKLKKRSLSEKKRFLREIQILRSHPNIVLGVSEDDHLVLMWMEGGDLPDY 88  
QY 60 SENARDSFIPVGHVLTQKINVOIASGLATVLRKNITFCCLKSDNIIWASLDVKEHINIK 119  
DB 89 RENG-----LHISEKAKKIALQIRGLFVYLSHSGIVHDLKRENIL-----LDENGTVK 138  
QY 120 LSDYGISRQ---SFHEGALGVEGTGPGYQAPFIRRIYVDKVMFSYGMVLYELLSGQRP 176  
DB 139 IADFLARKLSSSEKLTITVGPPEYMAVSEVLEGREYSSKVDVMSIGVLYELLTGKDP 198  
QY 177 ALGHQLOIAKLSKGRVLPQ-----EVQFRRIQALMECWDTKRKPPLASV 230  
DB 199 FPGIDPLELFRKE--RPRRLPLPPNCSE-----LKDIKKCINKDPKRPFAKEIL 251  
QY 231 S 231  
DB 252 N 252

## RESULT 15

US-10-288-798-12  
Sequence 12, Application US/10288798  
Publication No. US20030207299A1  
GENERAL INFORMATION:  
APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B;  
APPLICANT: WALIA, Nandinder K.; HARALIA, April J.A.;  
APPLICANT: YAO, Montique G.; GANDHI, Ameena R.;  
APPLICANT: GURURAJAN, Rajagopal; DING, Li;  
APPLICANT: PATTERSON, Chandra; YU, Henry;  
APPLICANT: BAUGHN, Mariah R.; TRISOULEY, Catherine M.;  
APPLICANT: THORNTON, Michael; ELIOTT, Vicki S.;  
APPLICANT: LU, Yan; ISON, Craig H.;  
APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;  
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;  
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;  
APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;  
APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;  
APPLICANT: THANGAVELU, Kavitha; BIRFORD, Neil  
TITLE OF INVENTION: HUMAN KINASES  
FILE REFERENCE: PI-0209 USA  
CURRENT APPLICATION NUMBER: US/10/288,798  
PRIOR FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: PCT/US01/27219  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/240,542  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/238,389  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/236,499  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 60/234,902  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US 60/232,654  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: US 60/231,357  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: US 60/229,873  
PRIOR FILING DATE: 2000-08-31  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PERL Program  
SEQ ID NO 12  
LENGTH: 1097  
TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID No. US20030207299A1 55052990CD1

US-10-268-798-12

Query Match 7.0%; Score 267.5; DB 12; Length 1097;  
Best Local Similarity 20.5%; Pred. No. 1.4e-13;  
Matches 178; Conservative 114; Mismatches 310; Indels 267; Gaps 35;

QY 3 RHURATDAMKNEFEPROEASMLALOHPCIVALLIGISHP--LCFALPLAPLSSINTYLS 60  
DB 174 RHDPEDDISQTLINVAQKALFAMLNHPVIALRGVCLKEPNLCIMEFARGGGLNRYLS 233  
QY 61 ENARDSFTPLGMLTOKI---AYQIASGLAYLHK---NIIFCLKSDNLYWLSL--- 110  
DB 234 -----GRIIPDILVMAVQIARGMNYLLDEALVPIIHRLDKSNILLQKVEN 282  
QY 111 -DYKEHINIKLSYGISKROSFHGAIGVEGTGQYQAPETPRIVYDEKVMFSYGMVLYE 169  
DB 283 GDLNRI-LKITDFGLAREMHRITKXASAGTYAMMAPEVIRASMFSGSDVMSYGVLLME 341  
QY 170 LLSGORPALGHQLOIA-----KLSKGRVPLGQPEEVQFRRLQALMMECWDTRPEKRP 224  
DB 342 LUNGVEPRFGIDGLAVAYGAMNKLALPISTCEP-----FAKLMEDCMNPDPHSRP 394  
QY 225 LAISVVSQM-----KDPFA--TPMYELCCGQTAFFSSQGEYTVFWD-- 267  
DB 395 SFTNILDQLTTEESGFEMPKDSFHCLQDNWKHEI---QEMFDQLAKEXELRTWEEZ 450  
QY 268 -----GKEE--SRNYTVNTEKIME-----VQWCCGKMYSCQL-QVQRLM 308  
DB 451 LTPALQCKQOEELRRBOELARRBIDLERELNIIHQCOEKPRYKRRKGRKRL 510  
QY 309 TATEDQKIYI-----YTL-----KMCPLNTPQOALDTPAVVTCFLAVPIKNSY 354  
DB 511 KLDGNRISLSPDFQHKFTVQASPTMDKRSKLINSRSPASPTIIRLRAIQLTPESS 570  
QY 355 LV-----LAQLADGLVAVP----- 369  
DB 571 KTWGRSSVVPKEGEEERAKRKRTWGPGLQKELASGDEGLKSLVDYQWSSA 630  
QY 370 --VVRGTPKD-----SCSYLC-SHTANRSKFSI 394  
DB 631 PNLVKG-PRSSPALPGFTSLMEMEDSDSGSGESRLQHSPOSYLCIFPRGEDGDP 689  
QY 395 ADEDAQNPYPV-----KAMEVNSG--SEWYSNGPGLVYDC 431  
DB 690 SSDGIHEEPTPVNSATPQLTPNLSLKRGAHRRCEVALLGCAVLAATGLGFDLLEA 749  
QY 432 ASLEICRLLEP-----YMAPSVTSVVCSEGRGEVWCLDDKANSL 474  
DB 750 GKQQLPLEPEPPAAEEKRRREGLFQSSSRPRSTSPSRKLFKEEPMLLLGDPASL 809  
QY 475 VMYHSTYQLCARVFCGVSPFLRD-----MPPVRPLDTEPPAASHANPKVBEGDSI 526  
DB 810 TLLSLSSISECN---STRSLRSDSDDEIVVEMPVPEVA-PLSPCTHNP-----L 857  
QY 527 ADVSI-MYGEELGTOLLHQESLTDYCGMSYSSSP-----PRQ--AARSPSLSPSPA 577  
DB 858 VNVKVERFKEDPNQSLTPTHVTLTPSQSPSHRRTPSDGALKPETLLASRSPSSNGLSPS 917  
QY 578 -----SSSVPPSTDCEDSDMLHTPGAASDRSEHDLTPMDETFSOHLQAVKILAVRDLI 632  
DB 918 PGAGESSSSFLFFFPQGMKTPSPSRDGEFPRLDPNVVFP----- 963  
QY 633 WYPRRGDVIIVIGLEKDEAQRGVIANVL 661  
DB 964 -TPRRW-----NTQQDSTLERPKTLEFL 985

Search completed: December 14, 2003, 07:25:34  
Job time : 38 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## CM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 14, 2003, 07:21:06, Search time 123 Seconds

(without alignments)

2612.414 Million cell updates/sec

Title: US-09-836-392-21

Perfect score: 3822

Sequence: 1 MURHURADAMKPFSEFRQ.....IFYSYELGLACTRKR 728

## Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODEL=frame+ p2n model -DEV=xip  
-Q/cgcn2.1/USFTO\_spool\_p/US09836392/runat.12122003.142519.1075/app.query.fasta.1.903  
-DB=Issued\_Patents\_NA -QFMT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosome2 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MIVLEN=0 -MAXLEN=2000000000  
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-NO\_WMAP -LARGEDUERY -VEC\_SCORES=0 -WAT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-FAPEXT=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents NA: \*  
1: /cgcn2.6/ptodata/2/ina/5A.COMB.seq: \*  
2: /cgcn2.6/ptodata/2/ina/5B.COMB.seq: \*  
3: /cgcn2.6/ptodata/2/ina/6A.COMB.seq: \*  
4: /cgcn2.6/ptodata/2/ina/6B.COMB.seq: \*  
5: /cgcn2.6/ptodata/2/ina/PCUS.COMB.seq: \*  
6: /cgcn2.6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	856	22.4	526	4	US-09-387-212-10
2	856	22.4	526	4	US-09-948-802-10
3	257.5	6.7	3389	1	US-08-395-580-1
4	247	6.5	2770	4	US-08-426-509A-5
5	247	6.5	2770	4	US-08-232-545-5
6	247	6.5	2770	4	PCT-US95-05008-5
7	243.5	6.4	2827	4	US-08-493-723-1
8	243.5	6.4	7607	1	US-08-222-616-19
9	243.5	6.4	7607	4	US-08-446-648-19
10	243.5	6.4	7607	5	PCT-US95-04228-19
11	243	6.4	1365	3	US-09-221-235-6
12	243	6.4	1365	3	US-09-221-928-6

13	243	6.4	1365	3	US-09-221-527-6	Sequence 6, Appl1
14	243	6.4	1365	3	US-09-221-236-6	Sequence 6, Appl1
15	243	6.4	1365	3	US-09-221-416-6	Sequence 6, Appl1
16	243	6.4	1365	3	US-09-221-245-6	Sequence 6, Appl1
17	243	6.4	1365	3	US-09-163-115-6	Sequence 6, Appl1
18	243	6.4	1365	3	US-09-221-528-6	Sequence 6, Appl1
19	243	6.4	1365	3	US-09-553-553-6	Sequence 6, Appl1
20	243	6.4	1365	3	US-09-221-237-6	Sequence 6, Appl1
21	243	6.4	1365	3	US-09-221-237-6	Sequence 6, Appl1
22	243	6.4	1365	3	US-09-221-235-4	Sequence 4, Appl1
23	243	6.4	1365	3	US-09-221-235-4	Sequence 4, Appl1
24	243	6.4	1365	3	US-09-221-237-4	Sequence 4, Appl1
25	243	6.4	1365	3	US-09-221-237-4	Sequence 4, Appl1
26	243	6.4	1365	3	US-09-221-237-4	Sequence 4, Appl1
27	243	6.4	1365	3	US-09-221-237-4	Sequence 4, Appl1
28	243	6.4	1365	3	US-09-221-237-4	Sequence 4, Appl1
29	243	6.4	1365	3	US-09-221-237-4	Sequence 4, Appl1
30	243	6.4	1365	3	US-09-221-237-4	Sequence 4, Appl1
31	243	6.4	1365	3	US-09-221-237-4	Sequence 4, Appl1
32	241	6.3	3425	1	US-08-205-018-1	Sequence 1, Appl1
33	238	6.2	2595	2	US-08-469-537A-77	Sequence 77, Appl1
34	238	6.2	3358	2	US-08-469-537A-104	Sequence 104, App
35	237.5	6.2	2016	3	US-09-132-118-1	Sequence 1, Appl1
36	237.5	6.2	2617	3	US-09-161-443-1	Sequence 1, Appl1
37	236	6.2	2890	1	US-07-928-464-1	Sequence 1, Appl1
38	236	6.2	2890	5	PCT-US93-07347-1	Sequence 1, Appl1
39	236	6.2	3033	1	US-08-003-111B-1	Sequence 1, Appl1
40	236	6.2	3033	1	US-08-261-432-1	Sequence 1, Appl1
41	234.5	6.1	2137	1	US-08-444-005-16	Sequence 16, Appl1
42	230	6.0	2598	4	US-09-417-197-110	Sequence 110, App
43	228.5	6.0	1788	4	US-09-529-279-14	Sequence 14, Appl1
44	228.5	6.0	1788	4	US-10-158-895-14	Sequence 14, Appl1
45	228.5	6.0	2268	1	US-08-444-005-14	Sequence 14, Appl1

## ALIGNMENTS

RESULT 1  
US-09-387-212-10  
Sequence 10, Application US/09387212A  
Patent No. 6309849  
GENERAL INFORMATION:  
APPLICANT: ROBINSON, KEITH E.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND  
FILE REFERENCE: NMI-090  
CURRENT FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 526  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: All occurrences of n indicate any nucleotide  
US-09-387-212-10

## Alignment Scores:

Pred. No.: 1.76e-74  
Score: 856.00  
Percent Similarity: 97.69%  
Best Local Similarity: 97.69%  
Query Match: 22.40%  
Length: 526  
Matches: 169  
Conservative: 0  
Mismatch: 1  
Indels: 3  
Gaps: 0

US-09-836-392-21 (1-728) x US-09-387-212-10 (1-526)

QY 99 AspleuysararapantileuValTTPSeleuAspVallyegluhistleantle 118  
DB 12 GACCTGAGTGGACACATTCGTGTGCTTGCACGTCAGGACACACATC 71  
QY 119 LysleuSerAspTyrGlyIleSerArgGlnSerPheHisGluGlyAlaGluValGlu 138

Db	72	AACGATCTGCATCAGCGGATTTCCAGGCGATCTTCATTCAGAGGGCGCCCTGAGCGCTGGAG	1311
Qy	139	GLYThrProGlyTyrGlnAlaProGlnIleArgProArgIleValTyrAspGlnIlyVal	158
Db	132	GGCACTCTCTGGTACCAAGGCGCCAGAGATCAGAGCCCTCGCATGTATATATAGAAAGATA	191
Qy	159	AspMetPheSerTyrGlnMetValLeuTyrGlnLeuLeuSerGlyGlnArgProAlaLeu	178
Db	192	GATATGTTCTCCATAGGAATGGAGGCTCTTCAGATTGCTGTCCAGGACAGCGCCGCACTG	251
Qy	179	GLYHisIleGlnLeuGlnIleAlaTyrLysIleuSerLysGlyIleArgProValLeuGly	198
Db	252	GGCCACACACAGCTCCAGATTGCCAAGAGCTGTCCAAAGGCAATCGCCCGGTTCTGGGG	311
Qy	199	GlnProGlnGlnValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTyrAspThr	218
Db	312	CAGCCGAGAGAAATGCGACTTCCGGGCACCTGCAGGCGCTATATATGAATGCTGTGGAGACT	371
Qy	219	LysProGlnIlyLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThr	238
Db	372	AAGCACAAGAGAGCAACACTGGCGCTGTGGTGGTGAAGCCAGATGAAGAGACCCGACTT	431
Qy	238	exaIaThrPheMetTyrGlnLeuCysGlyGlyGlnThrAlaPhePheSerSerGln	258
Db	432	TGCACACTTCATATATGAACCTGCGCTGTGGGAAGACAGACGCTCTTCTTCATCACCAG	491
Qy	258	IyGlnGlnIlyThrValValPheThrPaspGly	268
Db	492	GCCAGAGATACACTGTGGGTGTGTTTGGAGTGA	524

## RESULT 2

```

US-09-948-802-10
Sequence 10, Application US/09948802
Patent No. 6465232
GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
FILE REFERENCE: NMI-090
CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-948-802-10

```

Alignment Scores:

Pred. No.:	1,76e-74	length:	532
Score:	856.00	Matches:	16
Percent Similarity:	97.69%	Conservative:	0
Best Local Similarity:	97.69%	Mismatches:	1
Query Match:	22.40%	Indels:	3
DB:	4	Gaps:	0

US-09-836-392-21 (1-728) X US-09-948-802-10 (1-526)

QY 99 AspleuyserrapspaniilelevalITPSeLeAspVallyGlnH:stleleamle 118  
Db 12 GACCTGAAGTCGACAAACATTCTGGTGTGTCTCCCTTGACGTCAAGAGCACTCAACTC 71  
QY 119 LyAneuseraprryrcylilieseravrginseerPhniasciungylalaLeucliyValGlu 138  
Db 72 AAGCTATCTGCTACGGGATTTTGAAGCATCTCTTCATCAAGGAGGCCCTTACGCTGAG 133  
QY 139 GlyThrProGlyTyrglnalaProGluIleavrgProArgyleValTyraSpGluIyVal 156

Db	132	GGGACCTCCTGGCTACAGGGCCCCAGAGATCAAGGCTCGCATTTATATGATGAGAAAGTA	191
Qy	159	AspMetPheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnaGProAlaLeu	178
Db	192	GAAATATTTCTCTTAAGAAATGGTGTCTTACAGAGTTGCTGTGAGACAGCCCTTGACATG	251
Qy	179	GlyHisHisGluLeuGlnIleAlaLysLysLeuSerTyrGlyIleArgProValLeuGly	198
Db	252	GGGCACACACAGCTCCAGATTCACAGAAAGCTGTCCAAAGGCATCCGCCGGTTCGGGG	311
Qy	199	GlnProGluGluValGlnPheArgTyrLeuGlnAlaLeuMetMetGluCysTrpAspThr	218
Db	312	CACCCGAGAGAAAGTGTGAGTTCCGGGACCTGCAGCGAGGCTCATGAGAGAGTCTGGGACACT	371
Qy	219	LysProGluLysArgProLeuAlaLeuSerAlaVal-SerGlnMetLysAspProThrPn	238
Db	372	AAAGCCAGAAAGAGACCACTGGCCCTGTCCGTGTGTAAGCCAGATGAAGACCCGAACTTT	431
Qy	238	ealathrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePhe-SerSerGlnG	258
Db	432	TGCCACCTTCATGATGAAACTGTGCTGGAGAGACAGACGCTTCTTCATCACCAG	491
Qy	258	LysGlnLysTyrThrVal-ValPheTrpAspGly	268
Db	492	GCCAGAGATPACACTGTGGGTGTGTTGGAGATGGA	524

### RESULT 3

US-08-395-580-1  
; Sequence 1, Application US/08395580  
; Patent No. 5676945

**GENERAL INFORMATION:**

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1

```

## APPLICATION NUMBER: US/08/395,580

FILING DATE: herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/

## ATTORNEY/AGENT INFORMATION:

NAME: Rebecca L. Ralph (formerly Gaumond)

REFERENCE/DOCKET NUMBER: CH-04888

TELECOMMUNICATION INFORMATION:

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO:

LENGTH: 3389 base pairs

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: cDNA

## NAME/KEY: CDS

LOCATION: 99..2105





QY 348 ValIleLysAsnSerTyrlleuValIeu 357  
Db 2108 TTAAGCACACTAAACCAAGTATTTCCTT 2137

RESULT 5  
US-08-232-545-5  
Sequence 5, Application US/08232545  
Patent No. 6506578  
GENERAL INFORMATION:  
APPLICANT: Ulrich, Axel  
APPLICANT: Gishizsky, Mikhail  
APPLICANT: Sures, Iman G.  
TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,545  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)790-9090  
TELEFAX: (212)869-9741  
FAX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2770 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
US-08-232-545-5

Alignment Scores:  
Pred. No.: 6.6e-14 Length: 2770  
Score: 247.00 Matches: 99  
Percent Similarity: 44.32% Conservative: 65  
Best Local Similarity: 26.76% Mismatches: 129  
Query Match: 6.46% Indels: 78  
Gaps: 15

US-09-836-392-21 (1-728) x US-08-232-545-5 (1-2770)

QY 15 SerGluPheArgGlnGlnAlaSerMetLeuHleAlaLeuGlnHisProCysIleValAla 34  
Db 1179 AATGACTCTCGAGGGAGGCGACAGTATATAGAGAACTAAGACATCAAGCTTATCCAG 1238

QY 35 LeuIleGlyLeuSerIle-----HisProLeuGlyPheHleAlaLeuGlnLeuAlaProLeu 52  
Db 1239 CTTTATGCTGTTTGCACTTTAGAGATCCATTATTTATTACAGAGTTGATGAGACAT 1298

QY 53 SerSerLeuAsnThrValLeuSerGluAsnAlaArgSerSerPheIleProLeuGly 72  
Db 1239 GGAAGCTCGCAAGATATCTC-----CAAAATGACACTGATCAAAATTC----- 1343

QY 73 HisMetLeuThrGlnIleValIle-----AlaTyrlGlnIleHleAlaSerGlyLeuAlaTyrlleu 90  
Db 1344 ---CATCTGACTCAACAGGTGACATGCGCGACACAGTTCCTCTGGAATGGCTTATCTG 1400

QY 91 HisIlySerAsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValIrrPheSerLeu 110  
Db 1401 GAGTCTCGAAGTACATACATTCACAGATCTGGCTGCCAGAAAGTCTCTC----- 1448

QY 111 AspValLysGlnHisIleAsnIleLysLeuSerAspTyrlGlyIleSerArg----- 127  
Db 1449 ---CTTGATGACATAATATCTACAAAGTACAGATTTTGACCTTCCAGAGTTTAAAG 1505

QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140  
Db 1506 GTAGATATGAGACATCTATGATCTAGACACGAATAAAGCTGCCGTGAGAGTACT 1565

QY 141 ProGlyTyrlGlnAlaProGlnIleArgProArgIleValTyrlAspGlnLysValAspMet 160  
Db 1566 -----GGCCCGAAGCCATTCCTGAGTAAATTCAGCTTAAAGTCCAGATGTA 1613

QY 161 PheSerTyrlGlyMetValLeuTyrlGlyLeuLeuSer---GlyGlnArgProAlaLeuGly 179  
Db 1614 TGCTCATTTGGAAATCCTCTTTATGAAATCATTAATTATGCAAAATGCTTACAGTGT 1673

QY 180 HisIleGlnLeuGlnIleAlaLysLysLeuSerTyrlGlyIleArgProAlaLeuGlyGln 199  
Db 1674 ATGACAGTCCCGAGGATATCCAGATGCTGCCAAACTATAGA-----CTTCGGCA 1727

QY 200 ProGlnGlnValGlnPheArgArgLeuGlnAlaLeuMetGluCysTrpAspThrLys 219  
Db 1728 CCATCCCACTGCCA---CAGCAATTTTACACATCATCTTGGAGTCCGATGAGAG 1784

QY 220 ProGlnLysArgProLeuAlaLeuSerValIleSerGlnMetLysAspProThrPheAla 239  
Db 1785 CCTAAGGACGA-----CCTCATTTTGAG 1808

QY 240 ThrPheMetTyrlGluLeuCysCysGlyLysGlnThrAlaPhePhe----- 254  
Db 1809 ACACTGGTGGTGAAGCTTGAAGCTATTTGAAACGA-CTTCTATATTCAGATGCCAA 1867

QY 255 -----SerSerGlnGlyGlnGlyTyrlThrValValPheTrpAspGlyLysGln 270  
Db 1868 TAACTTCATAGATGAGACACTGAGAGATATCAAAATTAATAGTAGCAAAATTC 1927

QY 271 Glu-----SerArgAsnTyrlThrValIleAlaAsnThrGlnGlyLeuMetGlnValGln 288  
Db 1928 AATATATCCATTCMAAATATCAATGTTATCAAC----- 1960

QY 289 ArgMetCysCysProGlyMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTrp 308  
Db 1961 -----CAACTGCACATCATGTTATCTCGACA 1987

QY 309 ThrAlaThrGlnAspGlnLysIleTyrlTyrlThrLeuLysGly---MetCysProLeu 327  
Db 1988 TATTCAAAGTATGAGATTAAGTGGCCATGTTATGAAAAAGATTATTTTGCAATTTTA 2047

QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValIleThrCysPheLeuAlaValPro 347  
Db 2048 TTGACTGGCGACACATCGACAGACAGTCAGATCATATATATTTGCTCACTGCTCGAAAA 2107

QY 348 ValIleLysAsnSerTyrlleuValIeu 357  
Db 2108 TTAAGCACACTAAACCAAGTATTTCCTT 2137

RESULT 6  
PCT-US95-05008-5  
Sequence 5, Application PC/TUS9505008  
GENERAL INFORMATION:  
APPLICANT: Sugen, Inc.  
APPLICANT: 515 Galveston Drive  
APPLICANT: Redwood City, California 94063-4720  
APPLICANT: United States of America  
APPLICANT: Wissenschaften E.V.  
APPLICANT: Hofgarten Str. 2  
APPLICANT: Munchen 80539  
APPLICANT: Germany

```

/ TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: PC-DO/MS-DOS
/ OPERATING SYSTEM: PC-DO/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/05008
/ FILING DATE: 24-APR-1995
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 08/232,545
/ FILING DATE: 22-APR-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cornuzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7663-074
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 869-9741
/ TELEFAX: (212) 869-9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2770 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA
/ PCT-US95-05008-5

Alignment Scores:
Pred. No.: 6.6e-14 Length: 2770
Score: 247.00 Matches: 99
Percent Similarity: 44.32% Conservative: 65
Best Local Similarity: 26.76% Mismatches: 129
Query Match: 6.46% Indels: 78
DB: 5 Gaps: 15

US-09-836-392-21 (1-728) x PCT-US95-05008-5 (1-2770)
QY 15 SerGIuPheArgGlnGlnAlaSerMetLeuHisAlaLeuGlnHisProCySileValAla 34
DB 1179 AATGACTTCCTCGAGGAGGACAGATATGAAGAACTPAAGACATCCAAAGCTTATCAG 1238
QY 35 LeuIleGlyIleSerIle-----HisProLeuCySPheAlaLeuGlnLeuAlaProLeu 52
DB 1239 CTTTATGCTGTTGCACTTTAGAAAGATCCAAATTATATTATTAACAGAGTTGATGACAT 1298
QY 53 SerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGly 72
DB 1299 GGAAGCTCGCAAGAAATATCTC---CAAAATGCACTGATCAAAAATC----- 1343
QY 73 HisMetLeuThrGlnIleSile-----AlaTyrglnIleAlaSerGlyLeuAlaTyLeu 90
DB 1344 ---CATCTGACTCAACAGGTAGACATGGCGGACAGGTGGCTCTGGAATGGCCTATCTG 1400
QY 91 HisIleValAsnIleIlePheCyAspLeuIleuSerAspAsnIleLeuValTrpSerLeu 110
DB 1401 GAGTCGCGAAGTACTTACACAGAGATCTGCGTGCACAAATGCTC----- 1448
QY 111 AspValIleGlnHisIleAsnIleIleValSerAspTyrglyIleSerArg----- 127
DB 1449 ---GTTGGTGAACATATATCTACAAAGTAGACAGATTTTGGACTTGCACAGATTTTTAA 1505

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QY 128 -----GlnSerPheHisGluGlyAlaLeuGlnIleValGluGlyThr 140
DB 1506 GTAGATATAGAAACATCTATGATCTAGACAGAAATATAAGTCCGGTGAAGTGAAGT 1565
QY 141 ProGluIleValProGluIleArgProArgIleValIleArgIleValIleValIle 160
DB 1566 -----GGCCCGAAGCCATTGTAATTAATTAATTCAGCATTAAGTCCGATGTA 1613
QY 161 PheSerTyrglyMetValIleuTyrgluLeuLeuSer---GlyGlnArgProAlaLeuGly 179
DB 1614 TGGTCAATTGGAAATCCTCTTTATGAATATTAAGTATGCGCAAAATGCTTACAGTGT 1673
QY 180 HisIleGlnLeuGlnIleAlaIleValLeuSerIleGlyIleArgProValLeuGln 199
DB 1674 ATGACAGGTGCCGAGTAAATCCAGATGTTGCTCAAAACATATGA-----CTTCGCA 1727
QY 200 ProGluGluValAlaGlnPheArgArgLeuGlnAlaLeuMetMetGluCyStrPheThrIys 219
DB 1728 CCATCCAACTGTCCA---CAGCAATTTTACAAATCATGTTGAGAGTGTGGAATGCAAG 1784
QY 220 ProGluIleValProLeuAlaLeuSerValIleSerGlnMetIleAspProThrPheAla 239
DB 1785 CCTAAGGACGA-----CCTACATTTGAG 1808
QY 240 ThrPheMetTyrgluLeuCySylIleGlnThrAlaPhePhe----- 254
DB 1809 AACCTGCGTTGGAACTTGAAGACTATTTTGAACACGA-CCTTTCATATTCAGATGCAAA 1867
QY 255 -----SerSerGlnIleGlnIleTyrgluValIleValIlePheTrpAspGlyIleGln 270
DB 1868 TAAGTCAATTAAGATGAAGTCTGAGAAAGATATCAATATATAAAGTAGCAAAACAAATTC 1927
QY 271 Glu-----SerArgAsnIleTyrgluValIleValIleAsnThrGlnIleGlyLeuMetGluValGln 288
DB 1928 AAATPAATCCATTCCAAAATCAATGATATCAAC----- 1960
QY 289 ArgMetCySProGlyMetIleValSerGlyGlnLeuGlnValGlnArgSerLeuTrp 308
DB 1961 -----CAATGCAACATGATTTATCTGACA 1987
QY 309 ThrAlaThrGluAspGlnIleIleTyrglyIleTyrglyIleLeuIleGly---MetCySProLeu 327
DB 1988 TATTCACATGATAGATTAAGATGGCCATGATATTAAGAAATATATTATTTGCAATTTTA 2047
QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValIleValThrCySPheLeuAlaValPro 347
DB 2048 TTGACTGGCAACACTGCAAGACAGTCAAGTCAATATATGCTCAGCTGCTGGAATA 2107
QY 348 ValIleIleValAsnSerTyrgluValLeu 357
DB 2108 TTAAGCACACTAAACCAAGTATATTTTCIT 2137

RESULT 7
US-08-492-723-1
/ Sequence 1, Application US/08492723
/ Patent No. 6531296
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Edison T.
/ APPLICANT: Craven, Rolf J.
/ APPLICANT: Cance, William G.
/ TITLE OF INVENTION: NUCLEAR TYROSINE KINASE PAK
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Bell, Seltzer, Park & Gibson
/ STREET: PO Box 34009
/ CITY: Charlotte
/ STATE: NC 28234
/ COUNTRY: USA
/ ZIP: 28234
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/492,723  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sidley, Kenneth D.  
 REGISTRATION NUMBER: 31,665  
 REFERENCE/DOCKET NUMBER: 5470-121  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 INFORMATION FOR SEQ. ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2827 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 410..1924  
 US-08-492-723-1

Alignment Scores:  
 Pred. No.: 1,5e-13 Length: 2827  
 Score: 243.50 Matches: 99  
 Percent Similarity: 45.25% Conservative: 63  
 Best Local Similarity: 27.65% Mismatches: 117  
 Query Match: 6.37% Indels: 80  
 DB: 4 Gaps: 16

US-09-836-392-21 (1-728) x US-08-492-723-1 (1-2827)

QY 15 SerGlnPheArgGlnGlnAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34  
 DB 1223 AATGACTTCCTGAGGGAGGACAGACATTAAGAACTTAAGACATCCAAAGCTTATCAG 1282  
 QY 35 LeuIleGlyIleSerIle-----HisProLeuGlyPheAlaLeuGlnAlaProLeu 52  
 DB 1283 CTTTATGCTGTTGGACCTTAAAGATCCAAATTATTATTATTAACAGAGTTGATAGACAT 1342  
 QY 53 SerSerLeuAsnThrValLeuSerGlnAsnAlaArgAspSerPheIleProLeuGly 72  
 DB 1343 GGAAGCTCTCAAGAAATATCTC---CAAAATGACACTGATCAAAATC----- 1387  
 QY 73 HisMetLeuThrGlnIleIle-----AlaTyrglnIleAlaSerGlyLeuAlaTyLeu 90  
 DB 1388 ---CATCTACTCAACAGGTAGACATGGCGGACAGGTTGCTCTGAAATGGCCTATCTG 1444  
 QY 91 HisLeuLeuAsnIleIlePheCysAspLeuYsSerAspAsnIleLeuValTrpSerLeu 110  
 DB 1445 GAGTCTCGAAGCTACATTACAGAGATCTGGCTGCCAAGATGCTC----- 1492  
 QY 111 AspValIleGlnHisIleAsnIleLeuSerAspTyrgIleIleSerArg----- 127  
 DB 1493 ---GTTGGTGAACATAATATCTCAAGAGAGAGATTGGAAGTGCAGAGTTTAAAG 1549  
 QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140  
 DB 1550 GTAGATTAAGAAACATCTATATCATCAAGACACGAAATAAAGCTTACCGGTGAAGTGACT 1609  
 QY 141 ProGlyTyrglnAlaProGlnIleArgProArgIleValTyraAspGlnValAspMet 160  
 DB 1610 -----GCCGCCGAACCCATTGTAATTAATTAATTAATTAATTAATTAATTAATTA 1657  
 QY 161 PheSerTyrgIleMetValLeuTyrgIleLeuLeuSer---GlyGlnArgProAlaLeuGly 119  
 DB 1658 TGGTCAATTGGAACTCTCTTTATTAATAATCACTTATTTGGCAAAAGCCTTACAGTGGT 1717  
 QY 180 HisHisGlnLeuGlnIleAlaIleValLeuSerGlyIleArgProValLeuGlyGln 199

DB 1718 ATGACAGTGGCCAGGTATCCAGATGTGGCTCAAAACATATGA-----CTTCGCCAA 1771  
 QY 200 ProGlnGlnValGlnPheArgArgLeuGlnAlaLeuMetMetGlyCysTrpAspThrIle 219  
 DB 1772 CCATCAACAGTGGCA---CAGCATTTTACACATCATGTTGAGAGTCTGCAATGACAG 1828  
 QY 220 ProGlnIleArgProLeuAlaLeuSerValIleSerGlnMetIleAspProThrPheAla 239  
 DB 1828 CCTAAGAACCA-----CCTACATTTAG 1852  
 QY 240 ThrPheMetTyrgIleLeuCysCysGlyIleGlnThrAlaPhePhe----- 254  
 DB 1853 AACTGCGCTGGAACTTGAAGACTATTTTCAACACA-CCTTCATATTCAGATGCAAA 1911  
 QY 255 -----SerSerGlnGlyGlnGlnTyrgIleValValPheTrpAspGlyIleGln 270  
 DB 1912 TAACCTCATTAAGATGAACACAGCAAGAAATATCAATTAATAAAGTCAAAACAAATTC 1971  
 QY 271 Gln-----SerArgAsnTyrgIleValValAsnThrGlnIleGlyLeuMetGlnVal 287  
 DB 1972 AATATATATCATTCATCCAAATACAAATGATATATCAAC----- 2007  
 QY 288 GlnArgMetCysCysProGlyMetIleValSerCysGlnLeuGlnValGlnArgSerLeu 307  
 DB 2008 -----CACTGCACATCACTGTTATCTCTG 2031  
 QY 308 TrpThrAlaThrGlnAspGlnIleIleTyrgIleTyrgIleLeuGlyGly---MetCysPro 326  
 DB 2032 ACATATTTCAAGTATAGATTAAGTATTAAGTGGCCATGATTAATGAATAAAGTTATTTGTGATT 2091  
 QY 327 LeuAsnThrProGlnGlnAlaLeuAspThrProAlaValIleThrCysPheLeu 344  
 DB 2092 TTATGATCTGGCAACTGCTC---AGACACGTCAAGTGATATATATTTTCTCTC 2142

RESULT 8  
 US-08-222-616-19/c  
 Sequence 19, Application US/08222616  
 Patent No. 5635177  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, Brian D.  
 APPLICANT: Goeddel, David  
 APPLICANT: Lee, James M.  
 APPLICANT: Matthews, William  
 APPLICANT: Teal, Siao Ping  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd.  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/222,616  
 FILING DATE: 4-APR-1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/00586  
 FILING DATE: 22-JAN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/826935  
 FILING DATE: 22-JAN-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 821P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ. ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7607 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-222-616-19

## Alignment Scores:

Pred. No.	7,48e-13	Length:	7607
Score:	243.50	Matches:	99
Percent Similarity:	45.38%	Conservative:	63
Best Local Similarity:	27.73%	Mismatches:	117
Query Match:	6.37%	Indels:	79
DB:	1	Gaps:	16

US-09-836-392-21 (1-728) x US-08-222-616-19 (1-7607)

QY 15 SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34  
DB 2562 AATGACTTCCTGAGGAGGACAGATTAATGAAGACCTAAGACATCCAAAGCTTATCCAG 2503  
QY 35 LeuIleGlyIleSerIle-----HisProLeuCysPheAlaLeuGlnLeuAlaProLeu 52  
DB 2502 CTTTATGCTGTTGACCTTAGAAGATCCAAATTATATTATTACAGAGCTTATGAGCAT 2443  
QY 53 SerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGly 72  
DB 2442 GGAAGCTCCAGAAATATCTC---CAAAATGACACTGATCAAAATC----- 2398  
QY 73 HisMetLeuThrGlnIleIle-----AlaIleGlnIleAlaSerGlyLeuAlaIleLeu 90  
DB 2397 ---CATCTGACTCAACAGGTAGACATGGCGGACAGGTGCTCTGGAATGCTTACTG 2341  
QY 91 HisIleValAsnIleIlePheCysAspLeuIleSerAspAsnIleLeuValIleSerLeu 110  
DB 2340 GAGCTCGGAACTACACTTACAGAGATCTGCTGCCAGAAATGCTC----- 2293  
QY 111 AspValIleGlnHisIleAsnIleIleLeuSerAspIleIleSerArg----- 127  
DB 2292 ---GTTGCTGACATATATATCTACAAAGTAGAGATTGCTGCCAGATTGTTAAG 2236  
QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140  
DB 2235 GTAGATTAATGAACACTTATGATCTAGACACGAAATTAAGCTGCCGTAAGTGAAGT 2176  
QY 141 ProGlyIleGlnAlaProGlnIleArgProArgIleValIleAspGlnIleValAspMet 160  
DB 2175 -----GCGCCGAGAGCCATTCGTAGTAAATTAATTCAGATTAACTCCAGATGTA 2128  
QY 161 PheSerIleGlyMetValLeuIleIleValLeuSer-----GlyGlnArgProAlaLeuGly 179  
DB 2127 TGGTCATTGGAACTCTCTTTATGAATCACTTACTTATGGCAAAATCCCTTACAGTGT 2068  
QY 180 HisHisGlnLeuGlnIleAlaIleValIleSerIleGlyIleArgProValLeuGln 199  
DB 2067 ATGACAGGTGCCAGGTATCCAGATCTGCTCAAAACTAAG-----CTTCCGCA 2014  
QY 200 ProGlnGluValGlnPheArgArgIleGlnAlaLeuMetGlnCysIlePhePheIle 219  
DB 2013 CCATCCAACTGTCCA---CAGCAATTTTACAAATCATCATGTTGAGTGTGGAATGCAAG 1957  
QY 220 ProGlnIleArgProLeuAlaLeuSerValIleSerGlnMetIleAspProThrPheAla 239  
DB 1956 CTTAAGGAAGA-----CTTACATTTGAG 1933  
QY 240 ThrPheMetIleGlnLeuCysGlyIleGlnIleValIlePhePhe----- 254

DB 1932 ACACTGCGTGAACCTTGAAGACTATTTGAACAGA-CTTTCATATTCAGATGCCAA 1874  
QY 255 -----SerSerGlnGlyGlnGlyIleIleIleIleValIlePheIlePheIleGlyGly 270  
DB 1873 TAACCTCATTAAGATGAACACTGGAGAGAAATATCAAAATTAAGTGAACAAATTC 1814  
QY 271 Gln-----SerArgAsnIleIleIleValIleValIleIleIleIleIleIleIle 288  
DB 1813 AAATATATCATTCACAAATTAAGATTTATCAAC----- 1781  
QY 289 ArgMetCysProGlyIleMetIleValSerCysGlnLeuGlnValGlnArgSerIleIle 308  
DB 1780 -----CACTGCACATCACTTATCTGACA 1754  
QY 309 ThrAlaThrGluAspGlnIleIleIleIleIleIleIleIleIleIleIleIleIle 327  
DB 1753 TATTCAGATGATAGATATTAAGTGGCATGATATATGAAGATTTATTTGTCATTTTA 1694  
QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValIleIleIleIleIleIleIle 344  
DB 1693 TTGACTGGGCAACTGCG---AGACAGCTCAAGTGTATATATTTCTCTC 1646

## RESULT 9

US-08-446-648-19/c  
Sequence 19, Application US/08446648  
Patent No. 6311302  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Bennett, Brian D.  
APPLICANT: Goeddel, David  
APPLICANT: Lee, James M.  
APPLICANT: Matthews, William  
APPLICANT: Tsai, Siao Ping  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,648  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/222616  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0821P3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ. ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7607 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: linear  
US-08-446-648-19

## Alignment Scores:

Pred. No.	7,48e-13	Length:	7607
-----------	----------	---------	------

Score: 243.50  
 Percent Similarity: 45.38%  
 Best Local Similarity: 27.73%  
 Query Match: 6.37%  
 DB: 4  
 Matches: 99  
 Conservative: 63  
 Mismatches: 117  
 Indels: 79  
 Gaps: 16

US-09-836-392-21 (1-728) x US-08-446-648-19 (1-7607)

QY 15 SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34  
 DB 2562 AATGACTTCCTGAGGAGGACACAGATATGAAGAACTTAAGACATCCAAAGCTTATCCAG 2503  
 QY 35 LeuIleGlyIleSerIle-----HisProLeuCysPheAlaLeuGlnLeuAlaProLeu 52  
 DB 2502 CTTTATGCTGTTGACCTTACAGATCCAAATTATATATTATTAACAGGTTGATGAGACAT 2443  
 QY 53 SerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGly 72  
 DB 2442 GGAAGCTGCAAGAAATATCTC---CAAAATGACACTGATCAAAATC----- 2398  
 QY 73 HisMetLeuThrGlnIleIle-----AlaTrpGlnIleAlaSerGlyLeuAlaIleLeu 90  
 DB 2397 ---CATCTGACTCAACAGGTAGACATGGCGCACAGGTGCTCTGAAATGGCTTATCTG 2341  
 QY 91 HisLysLysAsnIleIlePheCysAspPheLysSerAspAsnIleLeuValTrpSerLeu 110  
 DB 2340 GAGTCTCGAATACATTCACAGAGATCTGGCTCCAGAAATGCTC----- 2293  
 QY 111 AspValLysGlnHisIleAsnIleLeuSerAspTrpGlyIleSerArg----- 127  
 DB 2292 ---GTTGTGGAACATATATATTAACAAGTACAAATTTGACACTTGCAAGATTTTAAAG 2236  
 QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140  
 DB 2235 GATGATATGAAGACATCTAGATCTAGACACAAATAAGCTCCGCTGAGTGAAGTGAAGT 2176  
 QY 141 ProGlyTyrglnAlaProGlnIleArgProArgIleValTrpAspGlnLysValAspMet 160  
 DB 2175 -----GGCCCCGAGACCATTCGTATATTAATTAATTCAGCATTAAGTCCAGTGA 2128  
 QY 161 PheSerTyrgIleMetValLeuTyrgIleLeuLeuSer-----GlyGlnArgProAlaLeuGly 179  
 DB 2127 TGGTCAITTTGGAAATCTCTTTAAGAAATCACTTAATGCAAAATGCTTAACTGCT 2068  
 QY 180 HisHisGlnLeuGlnIleAlaLysLeuSerIleArgProValLeuGlnGly 199  
 DB 2067 ATGACAGGTGCCCAAGTATCCAGATGTGGCTCAAAACATATGA-----CTTCCGCA 2014  
 QY 200 ProGlnGlnValGlnPheArgArgLeuGlnAlaLeuMetGluCysTrpAspThrLys 219  
 DB 2013 CCATCCAACTGTCCA---CAGCAATTTTAAACAACATCTTTGAGAGTGGATGCAAGAG 1957  
 QY 220 ProGlnLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAla 239  
 DB 1956 CCTAAGGAAACA-----CCTACATTGAG 1933  
 QY 240 ThrPheMetTyrgIleLeuCysCysGlyLysGlnThrAlaPhePhe----- 254  
 DB 1932 AACTGCGCTTGGAAACTGAAAGCTATTTGAAACAGA-CTCTTCATATTAGATGCAAA 1874  
 QY 255 -----SerSerGlnGlyGlnGlyTyrgIleValAlaPheThrAspGlyLysGln 270  
 DB 1873 TAACTTCATAGAGAACACTGAGAAAGAAATATCAAAATATTAAGTAAAGCAAAACAATTC 1814  
 QY 271 Gln-----SerArgAsnTyrgIleValValAlaAsnThrGlnLysGlyLeuMetGlnValGln 288  
 DB 1813 AAATATATCATTCCAAAATCAATGTTATCAAC----- 1781  
 QY 289 ArgMetCysCysProGlnMetLysValSerCysGlnLeuGlnValGlnArgSerIleTrp 308  
 DB 1780 -----CAACTGCAACATAGTTATCTGACA 1754  
 QY 309 ThrAlaThrGlnAspGlnLysIleTyrgIleTyrgIleLeuLysGly---MetCysProLeu 327

DB 1753 TATTCAGATGATAGATTAAGTTGGCCATGTATTATGAAAAAATATTATTCGATTTA 1694  
 QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValValThrCysPheLeu 344  
 DB 1693 TTGACTGGGCAACACTGC---AGACAGTCAAGGTATATATATTCTC 1646

# RESULT 10

PCT-US95-04228-19/c

Sequence 19, Application PC/TUS9504228

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
 APPLICANT: Bennett, Brian D.  
 APPLICANT: Goeddel, David  
 APPLICANT: Lee, James M.  
 APPLICANT: Matthews, William  
 APPLICANT: Tsai, Siao Ping  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
 NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: pacin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04228

FILING DATE:

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: 08/222616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 821P3PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 7607 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US95-04228-19

## Alignment Scores:

Pred. No.: 7,48e-13

Score: 243.50

Percent Similarity: 45.38%

Best Local Similarity: 27.73%

Query Match: 6.37%

DB: 5

Gaps: 16

US-09-836-392-21 (1-728) x PCT-US95-04228-19 (1-7607)

QY 15 SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34  
 DB 2562 AATGACTTCCTGAGGAGGACACAGATATGAAGAACTTAAGACATCCAAAGCTTATCCAG 2503  
 QY 35 LeuIleGlyIleSerIle-----HisProLeuCysPheAlaLeuGlnLeuAlaProLeu 52  
 DB 2502 CTTTATGCTGTTGACCTTACAGATCCAAATTATATATTATTAACAGGTTGATGAGACAT 2443

QY 53 SerSerLeuAenThrValIleuSerGluSerAlaArgAspSerPheIleProLeuGly 72  
 DB 2442 GGAAGCTGCAAGAAATATCTC---CAAAATGCACCTGATCAAAATC----- 2398  
 QY 73 HisMetLeuThrGlnLysIle-----AlaTyrGlnIleAlaSerGlyLeuAlaTyrLeu 90  
 DB 2397 ---CATCTGACTCAAGAGTACAGCATGGCGGACAGGTGGCTCTGGAAAGGAGCTTATCTG 2341  
 QY 91 HisLysLysAsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTyrSerLeu 110  
 DB 2340 GAGTCGGAACCTACATTCACAGAGATCTGGCTGCCAAGAAATGCTTC--- 2293  
 QY 111 AspValLysGlnHisIleAsnIleLysLeuSerAspTyrGlyIleSerArg----- 127  
 DB 2292 ---GTGGTGAACATATATCTACAAAGAGAGCAATTTGACCTGGCAGGTTTAAAG 2236  
 QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140  
 DB 2235 GTAGATATGAAGACATCTATGATCTTGAACCGAAATPAAAGTGGCGGAGAGTGAGT 2176  
 QY 141 ProGlyTyrGlnAlaProGlyIleArgProArgIleValTyrAspGlyLysValAspMet 160  
 DB 2175 -----GCCGCCAAGCCATTCGTAGTATATTAATTCACCATTAAGTCCGATGTA 2128  
 QY 161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSer---GlyGlnArgProAlaLeuGly 179  
 DB 2127 TGGTCATTTGGAATCCTCTTTATGAAATCATCTATTGCGAAATAGCCCTTACAGTGT 2068  
 QY 180 HisHisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGln 199  
 DB 2067 ATGACAGGTGCCAGGTATCCAGATGTTGGCTCAAAACTATAGA-----CTTCCCGCA 2014  
 QY 200 ProGluGlnValGlnPheArgArgLeuGlnAlaLeuMetGluCysTyrPheSerThrLys 219  
 DB 2013 CCATCCAACTGTCCA---CAGCAATTTTACAAACATCATGTTGGAGTGTGGAAGCGAG 1957  
 QY 220 ProGluLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAla 239  
 DB 1956 CTTAAGGAACGA-----CCTACATTTGAG 1933  
 QY 240 ThrPheMetTyrGluLeuLysCysGlyLysGlnThrAlaPhePhe----- 254  
 DB 1932 ACACCTGCGTTGGAACCTGGAAGACATATTTTGAACAGA-CCTTCATATTCAGATGCAAA 1874  
 QY 255 -----SerSerGlnGlyGlnGlyLysTyrThrValValPheTyrAspGlyLysGln 270  
 DB 1873 TAACCTCATTAAGATGAACACTGAGAGAGATATCAATATTAAGTGAACAAACAAATTC 1814  
 QY 271 Glu-----SerArgAsnTyrThrValValAsnThrGlyLysGlyLeuMetGluValGln 288  
 DB 1813 AATAATTCATTCACAAATACATGTTATCAAC----- 1781  
 QY 289 ArgMetCysCysProGlyMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTyr 308  
 DB 1780 -----CACTGCACATCAGTTATCTGACA 1754  
 QY 309 ThrAlaThrGlnAspGlnLysIleTyrIleTyrThrLeuLysGly---MetCysProLeu 327  
 DB 1753 TATTCAGATGATGATGATTAAGTTGGCATGTATTTGAAAAGATTAATTGTCGATTTTA 1694  
 QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValAlaTyrCysPheLeu 344  
 DB 1693 TTGACTGGGCAACACTGCT---AGGACATGCAAGGTGATATATATTTCTCTC 1646

QY 10 AlaleuLysAsnPheSerGluPheArgGlnGlnAlaSerMetLeuHisAlaLeuGlnHis 29  
 DB 127 GCTGAAAGAGCTCCCTCAAAATTAAGAAAGAGGCAAAATATCTAGTGTCTCACTAC 186  
 QY 30 ProCysIleValAlaLeuIleGlyIleSerIleHisProLeuCysPheAlaLeu----- 47  
 DB 187 AGAAACATCATCCAGTTTATGAGTATCTTGAACCTCCACATGATGATGTCACA 246  
 QY 48 GluLeuAlaProLeuSerSerLeuAenThrValIleuSerGluSerAlaArgAspSerSer 67  
 DB 247 GAATATGCTTCTCTGGATCATCTATGATTAATCACTAAGCA-----AGTGG 300  
 QY 68 PheIleProLeuGlnHisMetLeuThrGlnLysIleAlaTyrGlnIleAlaSerGlyLeu 87  
 DB 301 GAGATGATATGATCATCATATATGACTGG-----GCCACTGATATGCCAAAGGAATG 354  
 QY 88 AlaTyrLeuHisLysLys-----AsnIleIlePheCysAspLeuLysSerAspAsn 104  
 DB 355 CATATTTTACATATGAGGCTCTGTGAAGTGTATTCACAGAGACCTCANGTCAAGAAAC 414  
 QY 105 IleLeuValTyrSerLeuAspValLysGlnHisIleAsnIleLysLeuSerAspTyrGly 124  
 DB 415 GTGTATATGCTGCTGATGAGTA-----CTGAAGATCTGTGACTTTGGT 459  
 QY 125 IleSerArgGlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThrProGlyTyrGln 144  
 DB 460 GCCCTCTCGTCCATTAACCATACACACACATGCTCTGTGGAACTTTCCCATGAGATG 519  
 QY 145 AlaProGluIleArgProArgIleValTyrAspGlyLysValAspMetPheSerTyrGly 164  
 DB 520 GCTCAGAGATATCCAGAGATGCTCCGTGTGCAAAACTGTGACACATATCTCTATGG 579  
 QY 165 MetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlnHisIleGlnLeuGln 184  
 DB 580 GTGGTCTCTGGAAGATGCTTAACAGGAGAGTCCCTTAAAGGTTTGAAGGATTAACA 639  
 QY 185 IleAla---LysLysLeuSerLysGlyIleArgProValLeuGlnGlnProGluGlnVal 203  
 DB 640 GTAGCTTGCTTGAGTGAAGAAAAAGAGAGAG-----TTAACATTCACAAACAGTTCG 693  
 QY 204 GlnPheArgArgLeuGlnAlaLeuMetGluCysTyrPheSerThrLysProGlyLysArg 223  
 DB 694 CCC---AGAGATTTTGTGGAACCTTTCATCACTGAGTGGGAGCTGATGCCAAGAAACGG 750  
 QY 224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyr 243  
 DB 751 CCATATTCAGCAAAATCATTTCAATCTCTGAGTGCATGCAATATGACAGACCTTCTCT 810  
 QY 244 GluLeuCys 246

RESULT 11  
 US-09-221-235-6  
 ; Sequence 6, Application US/0921235  
 ; Patent No. 6043040  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan  
 ; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: NMT-050  
 ; CURRENT APPLICATION NUMBER: US/09/221,235

Db 811 GACAACTGT 819

RESULT 12  
US-09-221-928-6  
Sequence 6, Application US/09221928  
Patent No. 6121030  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: WNI-050  
CURRENT APPLICATION NUMBER: US/09/221,928  
CURRENT FILING DATE: 1998-12-28  
EARLIER APPLICATION NUMBER: 09/163,115  
EARLIER FILING DATE:  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1365  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1365)  
US-09-221-928-6

Alignment Scores:  
Pred. No.: 5,136-14 Length: 1365  
Score: 243.00 Matches: 71  
Percent Similarity: 49.79% Conservative: 50  
Best Local Similarity: 29.22% Mismatches: 104  
Query Match: 6.36% Indels: 18  
DB: 3 Gaps: 8

US-09-836-392-21 (1-728) x US-09-221-928-6 (1-1365)

QY 10 AAlMeTLYsAnPheserGluPheArGInGUAlaseMeTLeuHIsAlaLeuGInHIs 29  
Db 127 GCTGTAAAGAGCTCTCCAAATAGAGAGGCGCAAAATACCTGCTCTCAGCTCAC 186  
QY 30 ProCysIleValAlaLeuIleGlyIleSerIleHisProLeuCysPheAlaLeu----- 47  
Db 187 AGAACAATCATCCAGCTTTATGAGATTAATCTTCAACCTCCCAACTTGCAATGTCACAA 246  
QY 48 GluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerSer 67  
Db 247 GAATATGCTTCTCTGGATCCTCATGATTAATCACTAAGTAACAGTAACAGTA-----AGTGAG 300  
QY 68 PheIleProLeuGluHisMeTLeuThrGlnUlyIleAlaTyrgInIleAlaSerGlyLeu 87  
Db 301 GAGATGATATGATGATCAATTAATGACTCG-----GCCACTGATGAGCCAAAGAGATG 354  
QY 88 AlaTyrgInHisLysLys-----AsnIleIlePheCysAspLeuLysSerAspAsn 104  
Db 355 CATATTATTAATATGAGAGCTCTGTCAGAGTGATTCACAGAGAGCTCAAGTCAAGAAAG 414  
QY 105 IleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeuSerAspTyrgIy 124  
Db 415 GTTGTATAGCTGCTGATGAGTA-----CTGAAGATCTGTGACTTTGGT 459  
QY 125 IleSerArgInSerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrgIn 144  
Db 460 GCCTCTGCTCCATTAACATTAACAACACATGCTTGTTGTTGAATTTCCCATGGAG 519  
QY 145 AlaProGluIleArgProArgIleValTyrgPglLysValAspMetPheSerTyrgIy 164  
Db 520 GCTCCAGAGATTATCCAGAGCTCTCCTGTGTCAAACTTGTAACAACATTCCTATGTGT 579  
QY 165 MetValLeuTyrgLysLeuSerGlyLysArgProAlaLeuGluGlyHisGlnLeuGln 184  
Db 580 GTGGTTCTCTGGAGATCTTAACAAGAGAGTCCCTTTAAAGTTTGGAGAGATTACAA 639  
QY 185 IleAla---LysLysLeuSerLysGlyIleArgProValLeuGluGlnProGluGlnVal 203

Db 640 GATGCTGGCTTTGAGGAGAAAAACAGAGAG-----TTAACCATTTCCAAAGCTTGC 693  
QY 204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg 223  
Db 694 CCC---AGAGTTTGTGTAAGCTTTTACATCAAGTGTGGAGACTGATGCGAAGAAACGG 750  
QY 224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyrg 243  
Db 751 CCATCATTCAGCAAAATCAATTCATCTGAGATGCATGCAATGACACAGAGCTTCTCT 810  
QY 244 GluLeuCys 246  
Db 811 GACAACTGT 819

RESULT 13  
US-09-221-527-6  
Sequence 6, Application US/09221527  
Patent No. 6146832  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: WNI-050  
CURRENT APPLICATION NUMBER: US/09/221,527  
CURRENT FILING DATE: 1998-12-28  
EARLIER APPLICATION NUMBER: 09/163,115  
EARLIER FILING DATE:  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1365  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1365)  
US-09-221-527-6

Alignment Scores:  
Pred. No.: 5,136-14 Length: 1365  
Score: 243.00 Matches: 71  
Percent Similarity: 49.79% Conservative: 50  
Best Local Similarity: 29.22% Mismatches: 104  
Query Match: 6.36% Indels: 18  
DB: 3 Gaps: 8

US-09-836-392-21 (1-728) x US-09-221-527-6 (1-1365)

QY 10 AAlMeTLYsAnPheserGluPheArGInGUAlaseMeTLeuHIsAlaLeuGInHIs 29  
Db 127 GCTGTAAAGAGCTCTCCAAATAGAGAGGCGCAAAATACCTGCTCTCAGCTCAC 186  
QY 30 ProCysIleValAlaLeuIleGlyIleSerIleHisProLeuCysPheAlaLeu----- 47  
Db 187 AGAACAATCATCCAGCTTTATGAGATTAATCTTGAACCTCCCAACTTGCAATGTCACAA 246  
QY 48 GluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerSer 67  
Db 247 GAATATGCTTCTCTGGATCCTCATGATTAATCACTAAGTAACAGTAACAGTA-----AGTGAG 300  
QY 68 PheIleProLeuGluHisMeTLeuThrGlnUlyIleAlaTyrgInIleAlaSerGlyLeu 87  
Db 301 GAGATGATATGATGATCAATTAATGACTCG-----GCCACTGATGAGCCAAAGAGATG 354  
QY 88 AlaTyrgInHisLysLys-----AsnIleIlePheCysAspLeuLysSerAspAsn 104  
Db 355 CATATTATTAATATGAGAGCTCTGTCAGAGTGATTCACAGAGAGCTCAAGTCAAGAAAG 414  
QY 105 IleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeuSerAspTyrgIy 124  
Db 415 GTTGTATAGCTGCTGATGAGTA-----CTGAAGATCTGTGACTTTGGT 459  
QY 125 IleSerArgInSerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrgIn 144

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DB 460 GCCTTCGGTTCATTAACCATTAACACACATGTCCTGGTGAACCTTCCCATGGATG 519
QY 145 AAlaProGluLeuArgProArgGlyLeuValTyrAspGluValAspMetPheSerTyrGly 164
DB 520 GCTCCAGAAAGTATACAGAGTCTCCCTGTCAGAAACTTGTGACACATATCTTATGGT 579
QY 165 MetValLeuTyrGluLeuLeuSerGlyInrProAlaLeuGlyHisHisGlnLeuGln 184
DB 580 GTGGTTCTCTGGAGATGCTAACAGGAGAGTCCCTTTAAAGGTTTGGAAAGATTACAA 639
QY 185 IleAla---LysLeuLeuSerLysGlyLeuArgProValLeuGlyGlnProGluGluVal 203
DB 640 GTAGCTTGCGCTGTAGTGGAAAAAACAGAGA-----TTAACATTCCAGAGAGTGC 693
QY 204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTyrPhePheTyrLysProGluLysArg 223
DB 694 CCC---AGAAAGTTTGGCTGAACTGTATCATCATGAGTGGAGAGTGAAGCAAGAAACGG 750
QY 224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyr 243
DB 751 CCATCATTCAGCAATATCTTTCAATCCTGAGATCCATGTCATTAATGACAGAGCTTCT 810
QY 244 GluLeuCys 246
DB 811 GACAAAGTGT 819

RESULT 14
US-09-221-236-6
/ Sequence 6, Application US/09221236
/ Patent No. 6146841
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
/ FILE REFERENCE: NMI-050
/ CURRENT APPLICATION NUMBER: US/09/221,236
/ EARLIER FILING DATE: 1998-12-28
/ EARLIER APPLICATION NUMBER: 09/163,115
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 1365
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: CDS
/ LOCATION: (1)..(1365)
US-09-221-236-6

Alignment Scores:
Pred. No.: 5,136-14 Length: 1365
Score: 243.00 Matches: 71
Percent Similarity: 49.79% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 104
Query Match: 6.36% Indels: 18
DB: 3 Gaps: 8

US-09-836-392-21 (1-728) x US-09-221-236-6 (1-1365)
QY 10 AlaMetLysAsnPheserGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHis 29
DB 127 GCTGTAAAGAGCTCTCTCAAAATAGAGAAAGGACGAAATACATCAAGTCTCAGTCAC 166
QY 30 ProCysIleValAlaLeuLeuLeuGlyLeuSerIleHisPheProLysCysPheAlaLeu----- 47
DB 187 AGAATCATCATCAAGTTTATGAGATTAATCTTGAACCTCCCAACTATAGGCAATTGTACA 246
QY 48 GluLeuAlaProLeuSerSerLeuSerThrValLeuSerGluAsnAlaArgAspSerSer 67
DB 247 GAATATGCTTCTCTGGAGTCACTCTATGATTACATTAACAGTAACAG-----AGTGAG 300
QY 68 PheIleProLeuGlyHisMetLeuThrGlnLysIleAlaTyrGlnIleAlaSerGlyLeu 87
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DB 301 GAGATGATATGATGATCATTAATGACTGG-----GCCACTGATGATGCCAAAGGATG 354
QY 88 AlaTyrLeuHisLysLys-----AsnIleIlePheCysAspLeuLysSerAspAsn 104
DB 355 CATATATTACATATAGAGGCTCCGTGCAAGGTATTCACAGAGACTCAAGTCAAGAAAC 414
QY 105 IleLeuValTyrPheSerLeuAspValLysGlnHisIleAsnIleLysLeuSerAspTyrGly 124
DB 415 GTTGTATTAGCTGCTGATGAGATA-----CTGAAGATCTGTACATTTGGT 459
QY 125 IleSerArgGlnSerPheHisGlnGluAlaLeuGlyValGluGlyThrProGlyTyrGln 144
DB 460 GCCTTCGGTTCATTAACCATTAACACACATATCTCGTTGGAACTTCCCATGGATG 519
QY 145 AAlaProGluLeuArgProArgGlyLeuValTyrAspGluValAspMetPheSerTyrGly 164
DB 520 GCTCCAGAAAGTATACAGAGTCTCCCTGTCAGAAACTGTCAGAACATATCTTATGGT 579
QY 165 MetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHisHisGlnLeuGln 184
DB 580 GTGGTTCTCTGGAGATGCTTAACAGGAGAGTCCCTTTAAAGGTTTGGAAAGATTACAA 639
QY 185 IleAla---LysLysLeuSerLysGlyLeuArgProValLeuGlyGlnProGluGluVal 203
DB 640 GTAGCTTGCGCTGTAGTGGAAAAAACAGAGA-----TTAACCATTCAGAGAGTGC 693
QY 204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTyrPhePheTyrLysProGluLysArg 223
DB 694 CCC---AGAAAGTTTGGCTGAACTGTATCATCATGAGTGGAGAGTGAAGCAAGAAACGG 750
QY 224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyr 243
DB 751 CCATCATTCAGCAATATCAATCTTCAATCCTGAGATCCATGTCATTAATGACAGAGCTTCT 810
QY 244 GluLeuCys 246
DB 811 GACAAAGTGT 819

RESULT 15
US-09-221-416-6
/ Sequence 6, Application US/09221416
/ Patent No. 6153417
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
/ FILE REFERENCE: NMI-050
/ CURRENT APPLICATION NUMBER: US/09/221,416
/ EARLIER FILING DATE: 1998-12-28
/ EARLIER APPLICATION NUMBER: 09/163,115
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 1365
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: CDS
/ LOCATION: (1)..(1365)
US-09-221-416-6

Alignment Scores:
Pred. No.: 5,136-14 Length: 1365
Score: 243.00 Matches: 71
Percent Similarity: 49.79% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 104
Query Match: 6.36% Indels: 18
DB: 3 Gaps: 8

US-09-836-392-21 (1-728) x US-09-221-416-6 (1-1365)
QY 10 AlaMetLysAsnPheserGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHis 29
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Db 127 GCTGTAAGAGAGCTCTCAAAATAGAGAAAGAGGAGAAATACTCACTGTCTCACTGAC 186  
QY 30 ProCysIleValAlaLeuIleGlyIleSerIleHisProLeuCysPheAlaLeu----- 47  
Db 187 AGAAACATCATCTCACTTTATGAGTATCTTGAACTCCCACTATGAGCATTTGCACA 246  
QY 48 GluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerSer 67  
Db 247 GAAATGCTCTCTGGATCACTATGATTAACATTAACAGTAACAGA-----AGTGA 300  
QY 68 PheIleProLeuGlyHisMetLeuThrGlnIleValIleAlaIleAlaSerGlyLeu 87  
Db 301 GAGATGATATGATGATCAATATGACCTG-----GCCACTGATGTAGCCAAAGAAATG 354  
QY 88 AlaIleLeuHisLeuLys-----AsnIleIlePheCysAspLeuLysSerAspAsn 104  
Db 355 CATTAATTTACATATGAGAGCTCTGTCAGAGTGATTCACAGAGACCTCAAGATCAAGAAAC 414  
QY 105 IleLeuValIlePheSerLeuAspValLysGluHisIleAsnIleLysLeuSerAspIleGly 124  
Db 415 GTTGTATATAGCTGCTGATGAGATG-----CTGAAGATCTGTGACTTTGGT 459  
QY 125 IleSerArgGlnSerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyIleGln 144  
Db 460 GCCTCTCGGTTCCATTAACCATCAACAACACACATGTCTGTTGGACTTCCCATGGATG 519  
QY 145 AlaProGluIleArgProArgIleValIleAspGluLysValAspMetPheSerIleGly 164  
Db 520 GCTCCAGAAAGTTATCCAGAGTCTCCCTGTGCAGAACTGTGACACATATTCCTATGGT 579  
QY 165 MetValLeuIleGlyLeuLeuSerGlyGlnArgProAlaLeuGlyHisIleGlnLeuGln 184  
Db 580 GTGGTTCTCTGGAGATGCTTAACAAGGAGGTCCCTTAAAGTTGGAAGATTACAA 639  
QY 185 IleAla--LysLysLeuSerLysGlyIleArgProValLeuGlyGlnProGluGluVal 203  
Db 640 GTAGCTGGCTGTGATGGAAGAAACAGAGAGA-----TTAACCATTCACAGCAGTTGC 693  
QY 204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg 223  
Db 694 CCC--AGAAAGTTTGTGAAGCTGTATCATCAGTGTGGAGCTGATGCCAAGAAACGG 750  
QY 224 ProLeuAlaLeuSerValIleSerGlnMetLysAspProThrPheAlaThrPheMetIle 243  
Db 751 CCATCATTCAGCAATCATTTCAATCCTGAGATCCATGTCAATGACACAGAGCCTTCT 810  
QY 244 GluLeuCys 246  
Db 811 GACAGATGT 819

Search completed: December 14, 2003, 07:28:19  
Job time : 154 secs

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_p2n model

Run on: December 14, 2003, 07:24:52 ; Search time 538 Seconds

(without alignments)  
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Title: US-09-836-392-21

Perfect score: 3822

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Searched: 2201672 seqs, 166179599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HAPSIZE=500 -MINLEN=0  
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## Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/us07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Match	Length	ID	Description
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1	3822	100.0	3496	10	US-09-836-392-8	Sequence 8, Appli
2	3579.5	93.7	7015	15	US-10-132-382-5	Sequence 5, Appli
3	3579.5	93.7	7093	15	US-10-132-382-1	Sequence 1, Appli
4	3579.5	93.7	7229	15	US-10-132-382-7	Sequence 7, Appli
5	3579.5	93.7	7307	15	US-10-132-382-3	Sequence 3, Appli
6	3325	84.4	3112	13	US-10-094-749-50	Sequence 50, Appli
7	856	22.4	526	15	US-10-121-925-10	Sequence 10, Appli
8	341.5	8.9	3052	13	US-10-115-482-47	Sequence 47, Appli
9	330.5	8.6	3040	13	US-10-115-482-49	Sequence 49, Appli
10	330.5	8.6	5457	13	US-10-335-6878-6	Sequence 6, Appli
11	330.5	8.6	5479	13	US-10-335-6878-1	Sequence 1, Appli
12	330.5	8.6	5817	13	US-10-335-6878-4	Sequence 4, Appli
13	307.5	8.0	3454	10	US-09-869-347-226	Sequence 226, App
14	307.5	8.0	3454	15	US-10-171-581-312	Sequence 312, App
15	307.5	8.0	3453	13	US-10-210-120-86	Sequence 86, Appli
16	296.5	7.8	3453	10	US-10-210-120-86	Sequence 1014, Ap
17	270.5	7.1	1662	10	US-09-338-8428-1014	Sequence 36, Appli
18	270.5	7.1	3538	13	US-10-288-798-36	Sequence 1, Appli
19	269.5	7.1	3111	14	US-10-014-882-1	Sequence 1, Appli
20	269.5	7.1	3518	14	US-10-014-882-3	Sequence 3, Appli
21	268	7.0	1428	10	US-09-338-8428-882	Sequence 882, App
22	266.5	7.0	5549	14	US-10-354-358-23	Sequence 23, Appli
23	260.5	6.8	3558	13	US-10-143-133-1	Sequence 903, App
24	259.5	6.8	1638	10	US-09-814-353-20138	Sequence 20138, A
25	257.5	6.7	3761	13	US-10-153-668-323	Sequence 323, App
26	256.5	6.7	3365	15	US-10-153-668-437	Sequence 437, App
27	256.5	6.7	3428	15	US-10-153-668-437	Sequence 482, App
28	253.5	6.6	6378	13	US-10-252-157-482	Sequence 8, Appli
29	251.5	6.6	2696	13	US-10-128-174-8	Sequence 9, Appli
30	251.5	6.6	2696	13	US-10-128-174-9	Sequence 10, Appli
31	251.5	6.6	2696	13	US-10-128-174-10	Sequence 1577, Ap
32	251	6.6	2211	10	US-09-938-8428-1577	Sequence 435, App
33	248.5	6.5	2696	13	US-10-128-174-6	Sequence 6, Appli
34	248.5	6.5	2696	13	US-10-128-174-2	Sequence 2, Appli
35	247.5	6.5	2696	13	US-10-128-174-4	Sequence 4, Appli
36	247.5	6.5	2696	13	US-10-128-174-5	Sequence 5, Appli
37	247.5	6.5	2696	13	US-10-128-174-7	Sequence 7, Appli
38	247.5	6.5	2696	13	US-10-128-174-8	Sequence 8, Appli
39	247	6.5	2770	9	US-09-977-260-5	Sequence 5, Appli
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41	247	6.5	2770	11	US-09-977-260-5	Sequence 1631, Ap
42	243.5	6.4	2863	10	US-09-954-456-1631	Sequence 16, Appli
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## ALIGNMENTS

RESULT 1  
US-09-836-392-8  
Sequence 8, Application US/09836392  
Patent No. US20020173458A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypept:  
FILE REFERENCE: PTO20P1  
CURRENT APPLICATION NUMBER: US/09/836,392  
CURRENT FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: PCT/US00/28066  
PRIOR FILING DATE: 2000-10-11  
PRIOR APPLICATION NUMBER: 60/159,542  
PRIOR FILING DATE: 1999-10-15  
PRIOR APPLICATION NUMBER: 60/165,914  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 60/189,027  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: Patentm Ver. 2.0  
SEQ ID NO 8  
LENGTH: 3496  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-836-392-8

## Alignment Scores:

Pred. No.: 0 Length: 3496  
Score: 3822.00 Matches: 728  
Percent Similarity: 100.00% Conserved: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-836-392-21 (1-728) x US-09-836-392-8 (1-3496)

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DB 82 GCCAGCATGCTGCACCGCTGCAGCACCCCTGCATCTGGCGCTCATGGCATCAGCATC 141  
QY 41 HisProLeuCysPheAlaLeuGlnIleValAlaProLeuSerSerLeuAsnThrValLeuSer 60  
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DB 202 GAGAACGCCAGACATTTCTTCTTTATCCCTGGAGCACATGCTCACCAAAAATAGCC 261  
QY 81 TyrGlnIleAlaSerGlyLeuValIleTyrLeuHisIleLysIleIlePheCysAspLeu 100  
DB 262 TACCATGCGCTCGGCGCTGGCTTACCTGCACAGAAACATCATCTCTGTGACCTG 321  
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DB 682 GAGAAAGCAGACCGCTGCCTGTGTGGGTGAGCCAGATGAAGAGACCCGACTTTGCCACC 741  
QY 241 PheMetTyrGlnLeuCysGlyIleGlnThrAlaPhePheSerSerGlnGlyGlnGlu 260  
DB 742 TTCATGATGAATGTGCTGTGGAGAGACAGACGCTTCTCTCATCCAGAGGCGAGAG 801  
QY 261 TyrThrValValPheTyrAspGlyLysGlnGluSerArgAsnIleTyrThrValValAsnThr 280  
DB 802 TACACCGTGTGTTTGGAGTGAAGAAAGAGAGTCCAGAACTACACGCTGTGAACA 861  
QY 281 GlnLysGlyLeuMetCysValGlnArgMetCysCysProGlyMetLysValSerCysGln 300  
DB 862 GAGAAAGGCTCTCATGAGGTGCAGAGGATGTGCTCCCTGGAGTGAAGTGAAGTGCAG 921

QY 301 LeuGlnValGlnArgSerLeuTyrThrAlaThrGlnAspGlnLysIleTyrIleTyrThr 320  
DB 922 CTCACAGTCCAGAAATCCCTGTGAGCAGCACCGAGAGACAGAAAATCTACACTACACC 981  
QY 321 LeuLysGlyMetCysProLeuAsnThrProGlnAlaLeuAspThrProAlaValAla 340  
DB 982 CTCAGAGGCAATGTGCTTAAACACACCCCAACAGGCTTGATCTCAGACTGTGCTG 1041  
QY 341 ThrCysPheLeuAlaValProValIleLysLysAsnSerTyrLeuValLeuAlaGlyLeu 360  
DB 1042 ACCGCTCTTGCCCGCTGTGATTAATAAAGAAATCTTACCTGAGCTTACAGGGGCTCC 1101  
QY 361 AlaAspGlyLeuValAlaValPheProValValArgGlyThrProLysAspSerCysSer 380  
DB 1102 GCCATGGGCTGTGGCTGTGTTCCTGGTGTGGGGGCGACCCCAAGACACACTCTCC 1161  
QY 381 TyrLeuCysSerHisIleAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg 400  
DB 1162 TACCTGTGCTCACACACAGCCACAGGTCCAGTTCCAGATTCGCGGATGAAGACGACCG 1221  
QY 401 GlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValIleTyr 420  
DB 1222 CAGAACCCCTACCCAGTGAAGCCATGAGTGTCAACAGCGCTCTGAGGTGTGATC 1281  
QY 421 SerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGlnIleCysArgArgLeu 440  
DB 1282 AGCATGGGCGGCGCTCTTGTATGATGACTGTGCTCCCTGAGATCTGCAGCGGCTG 1341  
QY 441 GluProTyrMetAlaProSerMetValIleSerValValLysSerSerGlnIleArgGly 460  
DB 1342 GAGCCCTACATGGCCCTCCATGTTACGTACGTCTGTGACAGCTCTGAGGGCAGAGG 1401  
QY 461 GlnGluValValIleTyrCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480  
DB 1402 GAGAGGTGCTGTGTGTGCTGTGACAGAACGCCACTCTTGATGATGACCTCCACC 1461  
QY 481 ThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe 500  
DB 1462 ACCCTACAGCTGTGTGCGGGATCTTCTGCGGGGTCCCGACGCCCTCAGAGGACATGTT 1521  
QY 501 ProValArgProLeuAspThrGlnProProAlaAlaSerHisIleThrAlaAsnProLysVal 520  
DB 1522 CCGTGTGCGCCCTTGGACAGAAACCCCGGACGCCACACGCGCAACCCAAAGGTC 1581  
QY 521 ProGlnGlyAspSerIleAlaAspValSerIleMetTyrSerGlnGlnLeuGlyThrGln 540  
DB 1582 CCTGAGGGGACTCCATGCGGAGCGTGAAGATCATGTACGTGAGAGCTGGGACGACAG 1641  
QY 541 IleLeuIleHisGlnGlnLeuSerLeuThrAspTyrCysSerMetSerTyrSerSerSer 560  
DB 1642 ATCCGTGATCCACCGGAATCATCATGACTACTGCTCCATGTCTCTTACTCTCATATC 1701  
QY 561 ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer 580  
DB 1702 CCACCCCGCCAGGCTGCCAGGTCCCTCCCTCAAGCTCCCGACGCTCCAGCAATTTCTTC 1761  
QY 581 SerValProPheSerThrAspCysGluAspSerAspMetLeuHisIleTyrProGlyValAla 600  
DB 1762 AGTGTGCTTCTCCACCGACTGAGAGACTCAGACATGTATATAGCCCGGTGTGCTCC 1821  
QY 601 SerAspArgSerGlnHisAspLeuThrProMetAspGlyIleThrPheSerGlnHisLeu 620  
DB 1822 TCCGACAGGTCTGACATGACCTTACCCCATGACCGGAGACCTTCAACGACGACCTG 1881  
QY 621 GlnAlaValLysIleLeuAlaValArgAspLeuIleTyrValProArgArgGlyGlyAsp 640  
DB 1882 CAGGCGGTGAAGATCTCCGCTCAGAGACTCTATTGGGTGCCAGCGCGGTGAGAT 1941  
QY 641 ValIleValIleGlyLeuGlnLysAspSerGlnLysArgGlyArgValIleAlaVal 660  
DB 1942 GTTATGTCATTTGGCTGTGAGAAAGATTTCTGAAGCCAGAGGGGCGAGATTCCTCC 2001  
QY 661 LeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaValAlaLys 680

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Db      2002 TTTAAAGCCCGAGAGCTGACCTCGCATGGCGGTGCTGCTGAGTACGCTGCGCTGCGCAAG 2061
Qy      681 AsPthValValCysThrPheGluSngLuanThrGluTyrCysLeuAlaValTyrArg 700
Db      2062 GACACGTGTGTGTGACCTTTGAAAATGAAAACAGAGAGTGTGTGCTGGCCGTGAGG 2121
Qy      701 GLYTRPGIYAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu 720
Db      2122 GGCTGGGGCGCCAGGAGTTCACATTTTCTTACAGTCTCTACAGAGAGTGGCCGGCTG 2181
Qy      721 GLuAlaCysThrArgGlySarArg 728
Db      2182 GAGGCTTGCACTCGCAAGAGAGG 2205

RESULT 2
US-10-132-382-5
; Sequence 5, Application US/1012382
; Publication No. US20030045699A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS
; FILE REFERENCE: SCH-1811
; CURRENT APPLICATION NUMBER: US/10/132,382
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7015
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-132-382-5

Alignment Scores:
Pred. No.: 0 Length: 7015
Score: 3579.50 Matches: 688
Percent Similarity: 94.51% Conservative: 0
Best Local Similarity: 94.51% Mismatches: 1
Query Match: 93.66% Indels: 39
DB: 15 Gaps: 1

US-09-836-392-21 (1-728) X US-10-132-382-5 (1-7015)

Qy      1 MetLeuArgHisLeuAlaValThrAspAlaMetGlyAsnPheSerGluPheArgGlnGlu 20
Db      4124 ATGCTGAGGACCTCGGGCCACCGATGCCATGAGAGACTTCTCGAGTTCCGGCAGAG 4183
Qy      21 AlaSerMetLeuHisAlaLeuGlnHisSerProCysIleValAlaLeuIleGlyIleSerIle 40
Db      4184 GCCAGCATGCTCAACGGCGCTGACAGACCCCTGCATCGTGGCGCTCATCGCATCAGCATC 4243
Qy      41 HisProLeuGlyPheHisAlaLeuGlnHisSerProCysIleValAlaLeuIleGlyIleSer 60
Db      4244 CACCGCTCTGCTTGGCCCTGAGCTCGCGCGCTCAGCACCTCAACACCGCTCTGCC 4303
Qy      61 GluAsnAlaArgAspSerSerPheIleProLeuGlnHisMetLeuThrGlnIleValAla 80
Db      4304 GAGAACGCCAGAGATTTCTTCTTATACCTCGGACACATGCTCAACCAAAAATAGCC 4363
Qy      81 TyrGlnIleAlaSerGlyLeuAlaTyrLeuHisIleGlyAsnIleIlePheCysAspLeu 100
Db      4364 TACCAAGATCGCTCGGGCGCTGGCTTACCTGCAACAGAAAACATCATCTTCTGAGCTG 4423
Qy      101 LysSerAspAsnIleLeuValThrSerLeuAspValIleGlnHisIleAsnIleValLeu 120
Db      4424 AAGTCGAGCAACATCTGTGTGTGTCCTTACGTCAGGAGACACATCAATCAATCACTA 4483
Qy      121 SerAspTyrGlyIleSerArgGlnSerPheHisGlnGlyAlaLeuGlyValGluGlyThr 140
Db      4484 TCTGACTACGGGATTTTCAGGAGATTCATTCATGAGGGCGCCCTAGGCGTGAAGGACT 4543
Qy      141 ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluIleValAspMet 160

Db      4544 CCTGGCTACAGCCGCCAGAGATACAGCCCTCGCATTTGTATATGATGAGAGCTAGATATG 4603
Qy      161 PheSerTyrGlyMetValLeuTyrGluLeuSerGlyGlnArgProAlaLeuGlyHis 180
Db      4604 TTCTCTATGAGATATGTCCTCTACAGAGTTGCTGTACAGACAGCCCTCGACCTGAGGCGAC 4663
Qy      181 HisGlnLeuGlnIleAlaValLeuLeuSerIleGlyIleArgProValIleGlnGlnPro 200
Db      4664 CACCGACTCCAGATTTGCCAGAGAGCTGTCCAGAGGACATCCGCCCGCTTCTGGGGCAGCCG 4723
Qy      201 GluIleValGlnPheArgArgLeuGlnAlaLeuMetGlnCysTrpAspThrLysPro 220
Db      4724 GAGGAAGTGCAGTTCCGGCGACTCAGAGCGCTCATGATGAGTGTCTGGACACTAAGCCA 4783
Qy      221 GlyArgArgProLeuAlaLeuSerValIleSerGlnMetLysAspProThrPheAlaThr 240
Db      4784 GAGAAAGCAACGCTGCGCTGTCTGCTGTGAGCCAGATGAGAGGCCAGCCGACTTTGGCCACC 4843
Qy      241 PheMetTyrGluLeuGlyCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGlu 260
Db      4844 TTCATGATGAACTGTGTGTGGAGACAGACAGCTTCTTCTCATCTCCAGGCGCAGAG 4903
Qy      261 TyrThrValValPheTyrAspGlyLysGlnGlnSerArgAsnTyrThrValAlaSerThr 280
Db      4904 TACACCGGTGTGTGTGGAGTGAAGAGAGAGTCCAGAACTACACAGCGGTGTGAACACA 4963
Qy      281 GluLysGlyLeuMetGluValGlnArgMetCysCysArgProGlyMetLysValSerCysGln 300
Db      4964 GAGAAAGGCTCTCATGAGAGTGCAGAGATGTGCTGCTGCTGAGTGAAGAGTGAAGTCCAG 5023
Qy      301 LeuGlnValGlnArgSerLeuTyrThrAlaThrGlnAspGlnLysIleTyrIleTyrThr 320
Db      5024 CTCAGGTCCAGAGATCCCTGTGAGACAGCACCCAG----- 5059
Qy      321 LeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValVal 340
Db      5059 ----- 5059
Qy      341 ThrCysPheLeuAlaValProValIleLysHisAsnSerTyrLeuValLeuAlaGlyLeu 360
Db      5060 -----AATTCCTACCTGGTCTTACGGGCGCTC 5086
Qy      361 AlaAspGlyLeuValAlaValPheProValValAlaArgGlyThrProLysAspSerCysSer 380
Db      5087 GCCATGCGCTGTGGGTGTGTTCCTCCGTGTGCGGGAGCCCAAGAGACACTCTCTCC 5146
Qy      381 TyrLeuGlySerHisIleThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg 400
Db      5147 TACCTGTCTCAGACACAGACCAAGAGTCCAACTTCAGCATCCGCGATGAAGCGACCG 5206
Qy      401 GlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTyrTyr 420
Db      5207 CAGAACCTCTACCCAGTGAAGGCGCATGAGGTGTCAACAGCGCTCTGTGAGTGTGTAC 5266
Qy      421 SerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGlnIleCysArgArgLeu 440
Db      5267 AGCATGAGGCGGCGCTCTTGTTCATGATGTGTCTCTCCCTGAGATCTGAGGCGGCTG 5326
Qy      441 GluProTyrMetAlaProSerMetValThrSerValValCysSerSerGlnGlyArgGly 460
Db      5327 GAGCCCTACATGCGCCCTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 5386
Qy      461 GluIleValValTyrCysLeuAspAspValAlaAsnSerLeuValMetTyrHisSerThr 480
Db      5387 GAGGAGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5446
Qy      481 ThrTyrGlnLeuGlyAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe 500
Db      5447 ACCTACAGAGTGTGTGCGCGGTACTTCTGCGGGGTCCCGACCCCTCAGGAGCATGTTT 5506
Qy      501 ProValArgProLeuAspThrGlnProProAlaAlaSerHisIleThrAlaAsnProLysVal 520
Db      5507 CCGGTGGGCGCTTGTGACAGGAAACCCCGGACAGCCACAGGACCAACCAAGAGTGT 5566
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QY 521 ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGln 540  
 Db 5567 CCGAGGGGGAGCTCCATCCGGAGCGTACATCATGATGAGGAGCTGGGACCCAG 5626  
 QY 541 IleLeuIleHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer 560  
 Db 5627 ATCTGATCCACAGGAATCACTACTACTACTACTACTACTACTACTACTACTACTACTACT 5686  
 QY 561 ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer 580  
 Db 5687 CCACCCCGCAGGCTCCAGGCTCCCGCTCAAGCTCCCGAGCTCCCGCAAGTCTTCC 5746  
 QY 581 SerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGluAlaAla 600  
 Db 5747 AGTGTGCTTTTCTCCACCGACTCCGAGACTCAGACATCTACATACGCCCGGTGCTGCC 5806  
 QY 601 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 620  
 Db 5807 TCCGACAGGCTGAGCATGACCTGACCCCATGAGCGGGAGACCTTCAGCCACGACCTG 5866  
 QY 621 GlnAlaValIleIleLeuAlaValArgAspLeuIleThrValProArgArgGlyValAsp 640  
 Db 5867 CAGGCCGTGAAGTCTCCGCTCAGAGACTCATTTGGGTCCCGAGCGCGGTGGAGAT 5926  
 QY 641 ValIleValIleGlyLeuGluLeuYAspSerGluAlaGlnArgGlyArgValIleAlaVal 660  
 Db 5927 GTTATCGTCATTGGCTGAGAGAGATTCTGGCGCCGACGCGGGCCGAGTATTCGCCGTC 5986  
 QY 661 LeuLeuValAlaArgGluLeuThrProHisGlyValLeuValAspAlaAlaValAlaVal 680  
 Db 5987 TTTAAAGCCCGAGAGCTGACTCCGATGGGTGGTGGATGCTGGCGGTGGGCAAG 6046  
 QY 681 AspThrValValCysThrPheGluAsnGluAsnThrGluTyrCysLeuAlaValIleThrArg 700  
 Db 6047 GACACTGTGTGTGCACTTTGAAAATGAAAACAGAGTGTGTCTGCGCTGAGAG 6106  
 QY 701 GlyTyrGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu 720  
 Db 6107 GGCTGGGGCGCCAGGAGTTCGACATTTTCTACGTCCTTACGAGAGTGGCGGCTG 6166  
 QY 721 GlnAlaCysThrArgPheArgArg 728  
 Db 6167 GAGGCTTGCACTGCAAGAGAG 6190

RESULT 3  
 US-10-132-382-1  
 ; Sequence 1, Application US/10132382  
 ; Publication No. US20030045699A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEISS, BERTRAM  
 ; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS  
 ; FILE REFERENCE: SCH-1811  
 ; CURRENT APPLICATION NUMBER: US/10/132,382  
 ; CURRENT FILING DATE: 2002-04-26  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 7093  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-132-382-1

Alignment Scores:  
 Pred. No.: 0 Length: 7093  
 Score: 3579.50 Matches: 688  
 Percent Similarity: 94.51% Conservatve: 0  
 Best Local Similarity: 94.51% Mismatches: 1  
 Query Match: 93.66% Indels: 39  
 DB: 15 Gaps: 1

US-09-836-392-21 (1-728) x US-10-132-382-1 (1-7093)

QY 1 MetLeuArgHisLeuArgAlaThrAspAlaMetLeuAsnPheSerGluPheArgGlnGlu 20  
 Db 4202 ATGTGAGGACCTGGCGGCGACGAGATGCATCAAGAACTTCTCCAGATTCCGCGAGGAG 4261  
 QY 21 AlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIle 40  
 Db 4262 GCCAGCATGCTGCACCGGCTGCAGACCCCTGCATCGTGGCGCTCATTCGGCATCACATC 4321  
 QY 41 HisProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSer 60  
 Db 4322 CACCGCTCTCTTGGCCCTGAGACTGCGCCGCTCAGCAGCTTCAACACCGTGTCTCC 4381  
 QY 61 GluAsnAlaArgAspSerPheIleProLeuGlyHisMetLeuThrGlnIleAla 80  
 Db 4382 GAGAACGCCAAGATTTCTCTTATACCCCTGGACACATCTCCACCAAAATAGCC 4441  
 QY 81 TyrGlnIleAlaSerGlyLeuAlaTyrLeuHisIleValAsnIleIlePheCysAspLeu 100  
 Db 4442 TACCGATGCGCTGGCGCTGGCTTACCTGCACAGAAACATCATCTTCTGTGACCTG 4501  
 QY 101 LysSerAspAsnIleLeuValIleThrSerLeuAspValIleGluHisIleAsnIleValLeu 120  
 Db 4502 AAGTGCACACATTTGTGTGTGTCTCCCTTGACGCTCAGAGACATCAATCAATACGTA 4561  
 QY 121 SerAspTyrGlyIleSerArgGlnSerPheHisGlnGlyAlaLeuGlyValGluGlyThr 140  
 Db 4562 TCTGACTACGGATTTTGAGGACATTCATTCATAGAGGCGCTTACGGCTGAGGGCACT 4621  
 QY 141 ProGluTyrGlnAlaProGluIleArgProArgIleValIleThrAspGluYAspMet 160  
 Db 4622 CTTGCTACACAGGCGCCAGAGATAGGCTTCGCTGATATATATGAGAGAGATGATG 4681  
 QY 161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnAspProAlaLeuGlyHis 180  
 Db 4682 TTCTCTATGAAAGTGTGCTCTAGATTCTGTGACGAGCAGGCGCTGCAGCGGCAC 4741  
 QY 181 HisGlnLeuGlnIleAlaValLeuLeuSerLeuGlyIleArgProValLeuGlyGlnPro 200  
 Db 4742 CACCAAGCTCCAGATTTGCCAAGAACTCTCCAAAGGCTCCGCGCGGTTCGGGGCAGCGG 4801  
 QY 201 GluGluValAlaGlnPheArgArgLeuGlnAlaLeuMetGluCysTrpAspThrLysPro 220  
 Db 4802 GAGAAAGTGCAGTTCGGCGCATCTGCAGCGCTCATATGAGAGTGTGTGACATTAAGCCA 4861  
 QY 221 GluYAspArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThr 240  
 Db 4862 GAGAAAGCAGACCGCTGCGCTGTCCGTGTGAGCGCAGATGAAAGACCCGACTTTTGCACCC 4921  
 QY 241 PheMetTyrGluLeuLeuCysGlyValGlnThrAlaPhePheSerSerGlnGlyGlnGlu 260  
 Db 4922 TTCTATGTGAATCTGTGTGTGTGGAGACAGACAGCTTCTTCTCATCCAGGCGCAGAG 4981  
 QY 261 TyrThrValAlaPheTrpAspGlyValGlnGluSerArgAsnTyrThrValAlaAsnThr 280  
 Db 4982 TACACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5041  
 QY 281 GluYAspGlyLeuMetGluValGlnArgMetCysCysProGluMetLysValSerCysGln 300  
 Db 5042 GAGAAAGGCTTCATGAGGTGCAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5101  
 QY 301 LeuGlnValAlaGlnArgSerLeuTyrThrAlaThrGluAspGlnIleTyrIleTyrThr 320  
 Db 5102 CTCGAGTCCAGAGATCCCTGTGTGACAGCCACCGAG----- 5137  
 QY 321 LeuYAspGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValAla 340  
 Db 5137 ----- 5137  
 QY 341 ThrCysPheLeuAlaValProValIleLeuYAsnSerTyrLeuValLeuAlaGlyLeu 360  
 Db 5138 -----AATCTTACCTGCTTACCGGCGCTC 5164  
 QY 361 AlaAspGlyLeuValAlaValPheProValValArgGlyThrProLysAspSerCysSer 380

Db 5165 GCCGATGGCTTGTGCTGTGTTTCCCGTGGTGGGCGACCCCAAGACAGACTGCTCC 5224  
 QY 381 TyrLeuCySerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg 400  
 Db 5225 TACCTGTGCTACACACACAGCAGGTCCAGTTCAGCATGCGAGTGAAGACGCAAG 5284  
 QY 401 GluAsnProTyrProValIleValAlaMetGluValAlaAsnSerGlySerGluValTyrTyr 420  
 Db 5285 CAGAACCCCTACCCAGTGAAGGCCATGGAGTGTGTCAACAGGGGCTCTGAGAGTCTGGTAC 5344  
 QY 421 SerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGluIleCysArgArgLeu 440  
 Db 5345 AGCAATGGCGCGGCTCTTGTGATCGACTGTGCTCCCTGGAGATCTGACAGCGGGCTG 5404  
 QY 441 GluProTyrMetAlaProSerMetValThrSerValValCysSerSerGluGlyArgGly 460  
 Db 5405 GAGCCTTACATGGCCCTCCATGGTTAGTCACTGATGAGTGTGAGCTGAGGGGAGAGG 5464  
 QY 461 GluGluValValTyrCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480  
 Db 5465 GAGGAGTGTGTGTGCTGTGATGACAGGCCAATCTCTGTGATGTACACTCCACC 5524  
 QY 481 ThrTyrGluLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe 500  
 Db 5525 ACCTACAGCTGTGTGCTCCGTAATCTTGCGGGGTCCCGACGCCCTCAGAGGACATGTTT 5584  
 QY 501 ProValArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProValVal 520  
 Db 5585 CCGGTGGGCGCTTGGACACGGAAACCCCGGACGACCCACAGCCCAAGCAAGGAGTG 5644  
 QY 521 ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGln 540  
 Db 5645 CCTGAGGGGAGACTCCATCGCGAGCGTACATGATCATGTACAGTGAAGAGACTGGCACCCAG 5704  
 QY 541 IleLeuIleHisGluGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer 560  
 Db 5705 ATCTGATCCACAGGAATCACTCACTGACTATGCTCATGTCTCTTACTTCTCATACC 5764  
 QY 561 ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer 580  
 Db 5765 CCACCCCGCCAGGCTGCCAGGTCCCTCTCAAGCCCTCCACACTCCCAAGCAAGTCTTCC 5824  
 QY 581 SerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyValAla 600  
 Db 5825 AGTGTGCCCTTCTCCACCGACGTCAGAGCATGACATGATACATACCCCGGTGCTGCC 5884  
 QY 601 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 620  
 Db 5885 TCCGACAGGTCTGAGCATGACTGACCCCATGACGGGGAGACCTTCAAGCCAGACCTTG 5944  
 QY 621 GlnAlaValIleValIleLeuAlaValArgAspLeuIleTyrValProArgArgGlyGlyAsp 640  
 Db 5945 CAGGCCGTGAAGATCTCGCTCCAGAGACCTCATTTGGGTCCCAAGCGGGGTGGAGAT 6004  
 QY 641 ValIleValIleGlyLeuGluLeuAspSerGluAlaGlnArgGlyArgValIleAlaVal 660  
 Db 6005 GTTATGTCATTTGGCTGGAGAGAGATTTCTGGCGGCCAGCGGGCGAGTATTTGCCGTC 6064  
 QY 661 LeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaAlaValAlaLys 680  
 Db 6065 TTAAAGCCCGAGAGCTGACTCGCATGGGGGTGCTGTGATGTGCGGTGTGGCAAG 6124  
 QY 681 AspThrValValCysThrPheGluLeuGluLeuThrGluTyrCysLeuAlaValTyrArg 700  
 Db 6125 GACACTGTTGTGTGACCTTTGAAAATGAAAACAGAGTGTGTGCGTGTGGAGG 6184  
 QY 701 GlyTyrGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu 720  
 Db 6185 GGCTGGGGCGCCAGAGGAGTTGACATTTTCTACAGCTCTCTACAGAGAGCTGGCGGCTG 6244  
 QY 721 GluAlaCysThrArgGlyArgArgArg 728

Db 6245 GAGGCTTGCACTCGCAAGAGAGG 6268  
 RESULT 4  
 US-10-132-382-7  
 / Sequence 7, Application US/10132382  
 / Publication No. US20030045699A1  
 / GENERAL INFORMATION:  
 / APPLICANT: WEISS, BERTRAM  
 / TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS  
 / FILE REFERENCE: SCH-1811  
 / CURRENT APPLICATION NUMBER: US/10/132,382  
 / NUMBER OF FILING DATE: 2002-04-26  
 / NUMBER OF SEQ ID NOS: 26  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 7  
 / LENGTH: 7229  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 US-10-132-382-7  
 Alignment Scores:  
 Pred. No.: 0 Length: 7229  
 Score: 3579.50 Matches: 688  
 Percent Similarity: 94.51% Conservative: 0  
 Best Local Similarity: 94.51% Mismatches: 1  
 Query Match: 93.66% Indels: 39  
 DB: 15 Gaps: 1  
 US-09-836-392-21 (1-728) x US-10-132-382-7 (1-7229)  
 QY 1 MetLeuArgHisLeuArgAlaThrAspAlaMetLysAsnPheSerGluPheArgGlnGlu 20  
 Db 4338 ATGCTGAGGACACTGGCGGCGCACCGAGTGCATGAAGAACTTCTCCGAGTCCGCGCAGAG 4397  
 QY 21 AlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIle 40  
 Db 4398 GCGACGATGCTGACGCGCTGACACACCCCTGATCTGTGGCGCTCATGCGCATGAGCATC 4457  
 QY 41 HisProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSer 60  
 Db 4458 CACCGGCTCTGCTTGGCTTGGAGCTGCGCGCTGACGAGCTGCAAGACCTCAACCGTGTGCTC 4517  
 QY 61 GluAlaAlaArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAla 80  
 Db 4518 GAGAACGCGCAGAGATTTCTCTTATACCCCTGGGACACATGCTCACCCAAAATAAGCC 4577  
 QY 81 TyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLysAsnIleIlePheCysAspLeu 100  
 Db 4578 TACCAATCGCTCGGCGCTGCTTACTCTGACACAGAAAACATCATCTTCTGTGACCTG 4637  
 QY 101 LysSerAspAsnIleLeuValTyrSerLeuAspValIleGluHisIleAsnIleLysLeu 120  
 Db 4638 AAGTCGACCAACATTTCTGTGTGTCTCCCTGACCTCAAGAGACATCAACATCAAGCTA 4697  
 QY 121 SerAspTyrGlyIleSerArgGlnSerPheHisGluGlyAlaLeuGlyValGluGlyThr 140  
 Db 4698 TCTGACTACGGGATTTGAGGCACTCATTCATAGAGGCCCTTAGCGCTGAGGGCACT 4757  
 QY 141 ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMet 160  
 Db 4758 CTGGCTACAGGCCCCAGAGATCAGGCTCGCATTTGATGATGAGAGGTAGATATG 4817  
 QY 161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHis 180  
 Db 4818 TTCTCTTATGGAATGTGTCTTACAGATGTCTGTCAAGACAGAGCGCCCTGCACTGGGCAAC 4877  
 QY 181 HisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValIleuGlyGlnPro 200  
 Db 4878 CACCAAGCTCCAGATTTGCCAAGAGACTCTCCAAAGGACATCCGCCGGTCTGGGGCAGCGG 4937  
 QY 201 GluGluValGlnPheArgArgLeuGlnAlaLeuMetMetLysCysTyrPhePheThrLysPro 220  
 Db 4938 GAGGAAGTGACGTTCCGGCGACATGACAGCGCTCATGATGAGTGTGGGCACTTAAGCCA 4997

QY	22	GLIYSAAGPProLeuAlaLeuSerValValSerGIuMetLeuAspProThrPheAlaThr	240
Db	4998	GAGAACCAACCGCTGCGCTCTCGCTGAGCCAGTAAAGAACCACTTTTCCACC	5057
QY	241	PheMetTyrGIuLeuCysCysGIYLYSGInThrAlaPhePheSerSerGIuGIu	260
Db	5058	TTCACTGATGAAGTGTGCTGTGGAGACAGACGCTTCTTTCATCCAGGGCCAGAG	5117
QY	261	TyrThrValValPheTrpAspGIYLYSGIuGLeuSerArgAsnTyrThrValValAsnThr	280
Db	5118	TACACCGCTGCTTTTGGGATGCAAAAGAGAGTCCAGAACTACACGGTGTGAACA	5177
QY	301	LeuGIuValAlaArgSerLeuTrpThrAlaThrGIuAspGIuMetLysTyrThr	320
Db	5238	CTCCAGGTCCAAAGATCCCTGTGACACGCCAGC-----	5273
QY	321	LeuLYSGIuMetCysProLeuAsnThrProGIuGlnAlaLeuAspThrProAlaValAla	340
Db	5273	-----	5273
QY	341	ThrCysPheLeuAlaValProValIleLysLYSAAsnSerTyrLeuValLeuAlaGIYLeu	360
Db	5274	-----AATTCTTACTGTGCTTACCGGGCTTC	5300
QY	361	AlaAspGIYLeuValAlaValPheProValValArgGIYThrProLYSAAspSerCysSer	380
Db	5301	GCCGAGGGGCTTTGTGGCTGTTCCTCCGTGTGGGGGACCCCAAGAGACGCTGCTCC	5360
QY	381	TyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGIuAspAlaArg	400
Db	5361	TAACCTGTGTCTACACAGACCAAGATCCAAAGTTCAGATCCCGATTAAGACCAACG	5420
QY	401	GIuAsnProTyrProValLYSGIuMetGIuValValAsnSerGIYSerGIuValTrpTyr	420
Db	5421	CAGAACCCCTTACCCAGTAAAGCCATGAGGTGTGTCAACGGCGCTCTAGCTGTGATC	5480
QY	421	SerAsnGIYProGIYLeuLeuValIleAspCysAlaSerLeuGIuIleCysArgArgLeu	440
Db	5481	AGGAAGGGGCGCGGCTCTTGTCTATGCACTGTGCTCCCTGTGAAGTCTGCAGCGGCTG	5540
QY	441	GIuProTyrMetAlaProSerMetValThrSerValLYSAsnSerGIuGIYArgLY	460
Db	5541	GAGCCCTCATGTGGCCCCCTCATGGTTACGTCAGTCTGTGCAGCTCTAGAGGCGAAGGG	5600
QY	461	GIuGIuValValTrpCysLeuAspAspLYSAIAsnSerLeuValMetTyrHisSerThr	480
Db	5601	GAGAGAGTGTCTGTGCTGTGAGTGAACAAGCCAACTCTGTGATGTACACTCCACC	5660
QY	481	ThrTyrGIuLeuCysAlaArgTyrPheCysGIYValProSerProLeuArgAspMetPhe	500
Db	5661	ACCTACCACTGTGTGGCCGGTACTTTCGCGGGTCCCCAGCCCTCCAGGACATGTTT	5720
QY	501	ProValArgProLeuAspThrGIuProProAlaAlaSerHisThrAlaAsnProLYSAI	520
Db	5721	CCGCTGGGCGCTTGTGACACGGAACCCCGGACGCCACACAGCGCCAAACCAAGGTG	5780
QY	521	ProGIuGIYAspSerIleAlaAspValSerIleMetLysSerGIuGIuLeuGIYThrGln	540
Db	5781	CTGAGAGGGGAGCTCATGTGGGACGTGACATCTATGACGTAGAGAGTGTGGACAGAG	5840
QY	541	IleLeuIleHisGIuGlnSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer	560
Db	5841	ATCTGTATCCACAGGAATCACTCACTGACTGATGCTCATGTCTTACTCTCATTC	5900
QY	561	ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer	580
Db	5901	CCACCCCGGACAGGCTGCAGAGTCCCCCTCAAGCTCCCAAGTCTCCCAAGATTTCTTC	5960

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QY      581  SerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyValAla 600
Db      5861  AGTGTGCTTTCTTCCACCTGCACTGCGAGCACTCAGACACTGCTTAATACGCCGGTGTGCTCC 6020
QY      601  SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 620
Db      6021  TCCGACAGGCTGTGACATGACCTTACCCCATGGACGGGAGAGACTTTCACCCAGCACTGT 6080
QY      621  GlnAlaValIleValIleLeuAlaValArgAspLeuLeuLeuValProArgArgGlyValAsp 640
Db      6081  CAGGCGCGGAAGATCTCCGCGCTGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGAT 6140
QY      641  ValIleValIleGlyLeuGlyLeuGlyAspSerGluAlaGlnArgGlyArgValIleAlaVal 660
Db      6141  GTTATCGTCATTTGGCTCTGAGAAAGATTTCTGGCGCCACGCGGGCGCAGTCAATGGCTGC 6200
QY      661  LeuValAlaArgGlyLeuLeuThrProHisGlyValLeuValAspAlaAlaValAlaVal 680
Db      6201  TTAAAGCCCGCAGAGCTGACCTCCGCACTGGGAGTCTGTGTGATGCTGTCCGTGTGGCAG 6260
QY      681  AspThrValValCysThrPheGluAsnGluAsnThrGluThrCysLeuAlaValAlaThrPar 700
Db      6261  GACACTGTGTGTGTCACCTTTGAAAAAGAAACACAGAGTGTGTGCTGTCCGCTGTGAGG 6320
QY      701  GlyTrpGlyAlaArgGlyIlePheAspIlePheThrGlnSerTyrluGluLeuGlyArgLeu 720
Db      6321  GGCTGGGGCGCCAGAGGAGTTGCAATTTTTCACAGTCTTAACAGAGAGAGTGGGGCGGCTG 6380
QY      721  GluAlaCysThrArgIleArgIleArg 728
Db      6381  GAGGCTTGCACTCCGAAAGAGAGG 6404

RESULT 5
US-10-132-382-3
; Sequence 3, Application US/10132382
; Publication No. US20030045699A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
FILE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
TITLE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 7307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-132-382-3

Alignment Scores:
Pred. No.: 0 Length: 7307
Score: 3579.50 Matches: 688
Percent Similarity: 94.51% Conservative: 0
Best Local Similarity: 94.51% Mismatches: 1
Query Match: 93.66% Indels: 39
DB: 15 Gaps: 1

US-09-836-392-21 (1-728) x US-10-132-382-3 (1-7307)
QY      1  MetLeuArgHisLeuArgAlaThrAspAlaMetIleAsnPheSerGluPheArgGln 20
Db      4416  ATGCTGAGGACCTGCGGGCCACCGCATGCCATGAAAGAACTTCTCCGAGTTCGGCAGAG 4475
QY      21  AlasertMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIle 40
Db      4476  GCCAGCAGTGCAGCGGCTGCACACACCCCTGCATCTGTGGGCTCATCGGCATCAGATC 4535
QY      41  HisProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSer 60
Db      4536  CACCCGCTCTCTCCGCTCGAGCTCGCGCGCTCAGACGCTCAACACCGTGTCTCTCC 4595
QY      61  GluAsnAlaArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnIleValAla 80

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Db      4596 GAGAACGCCAGAGATTCTTCTTATACCCCTGGAGACATGCTACCCAAAATATGCC 4655
Qy      81  TrrGlnIleAlaSerGlyLeuAlaTrrLeuHisIleGlySerValIleIlePheCysAspLeu 100
Db      4656 TACCGATGCTCGGGCTGCTGCTTACCTGACCAAGAAAACATCATCTTCTGTGACCTG 4715
Qy      101  LysSerAspAsnIleLeuValTrrSerLeuAspValIleGlyHisIleLeuValIleLeu 120
Db      4716 AAGTCGACAAACATTTCTGCTGCTGCTTACCTGACCAAGAACATCATCATCACTA 4775
Qy      121  SerAspTrrGlyIleSerArgIleSerPheHisGlyAlaLeuGlyValGlyIleThr 140
Db      4776 TCTGACTACGGGATTTCAGAGCAGTCATTCATGAGGGCGCCCTAGGGGTGAGGAGCACT 4835
Qy      141  ProGlyTrrGlnAlaProGlyIleArgProArgIleValTrrAspGlyLeuValAspMet 160
Db      4836 CTGGCTACCAAGGCCCAAGATCAGGCTGCTGCTGATGTAATGATGAGAGATGATATG 4895
Qy      161  PheSerTrrGlyMetValLeuTrrGlyLeuLeuSerGlyGlnArgProAlaLeuGlyHis 180
Db      4896 TTCTCTATGGAATGGTGTCTACAGATGGTGTCTGAGACAGCGCCCTGACCTGGCCAC 4955
Qy      181  HisGlnLeuGlnIleAlaAlaLeuLeuSerIleGlyIleArgProValLeuGlyGlnPro 200
Db      4956 CACACAGCTCCAGATTGCGCAAGAGCTGTCAGAGGCAATCCGCGGTTCTGGGGCAGCCG 5015
Qy      201  GlnGlyValAlaGlnPheArgTrrGlnGlnAlaLeuMetMetGlyCysTrrPheTrrThrPro 220
Db      5016 GAGAGATGCAAGTTCGGGCACTGACAGCGCTCATGATGAGTCTGGGACACTGAGCCA 5075
Qy      221  GlyLeuArgProLeuAlaLeuSerValIleSerGlnMetIleAspProThrPheAlaThr 240
Db      5076 GAGAACGCCAGCCCTGGCCCTGTGCTGCTGAGCCAGATGAAAGACCCGACTTTGGCCACC 5135
Qy      241  PheMetTrrGlyLeuCysGlyGlyGlnIlePhePheSerSerGlnGlyGlnGlu 260
Db      5136 TTCTATGTAATGAACTGTGCTGTGGGAGACAGACGCTTCTTCTCATCCAGGGCCAGAG 5195
Qy      261  TrrThrValIleValPheTrrPheAspGlyLeuGlnIleSerArgSerIleTrrThrValIleThr 280
Db      5196 TACACCGTGTGTTTGGATGGAAGAAAGAGTCCAGAACTACACGGTGTGTAACACA 5255
Qy      281  GlyLeuGlyLeuMetGlyValAlaGlnArgMetCysCysProGlyMetLeuValSerCysGln 300
Db      5256 GAGAAAGGCTCATGAGAGTGCAGAGAGATGCTGCTGGATGAAAGGTAGAGTGCAG 5315
Qy      301  LeuGlnValAlaGlnArgSerLeuTrrPheAlaThrGlnAspGlnIleTrrIleTrrThr 320
Db      5316 CTCGAGGTCCAGAGATCCCTGTGAGACGCCAGCCAG----- 5351
Qy      321  LeuLeuGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValVal 340
Db      5351 ----- 5351
Qy      341  ThrCysPheLeuAlaValProValIleLeuIleLeuValIleLeuAlaGlyLeu 360
Db      5352 -----AATTCTTACTGCTGCTTACGCGGCTTC 5378
Qy      361  AlaAspGlyLeuValAlaValPheProValValArgGlyThrProIleAspSerCysSer 380
Db      5379 GCGGATGGGCTGTGTGCTGTGTTTCCGTGTGCGGGGCAACCCAAAGGACAGCTGCTCC 5438
Qy      381  TrrLeuCysSerHisThrAlaAsnArgSerIlePheSerIleAlaAspGlyAspAlaArg 400
Db      5439 TACTGTGCTCACACACAGCCAAAGCTCCAAATTCACATTCGCGATGAAAGCGCACGG 5498
Qy      401  GlnAsnProTrrProValIleValIleValIleValIleAsnSerGlySerGlyValIleTrrThr 420
Db      5499 CAGAACCCCTAACCCAGTGAAGGCTGAGGCTGTCACACAGCGCTGAGGCTGTGCTAC 5558
Qy      421  SerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGlnIleCysArgArgLeu 440

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Db      5559 AGCAATGGGCGGGCTCCTTGTGATGACTGTGGCTCCCTGGAGATCTGACAGCGGCTG 5618
Qy      441  GluProTrrMetAlaProSerMetValIleSerValValIleSerSerGlyGlyArgGly 460
Db      5619 GAGCCCTACATGAGGCCCCCTCATGTGTACCTGATGCTGTGAGGCTCTGAGGCAAGGG 5678
Qy      461  GlnGlyValValIleTrrCysLeuAspAspValAlaAsnSerLeuValMetTrrHisSerThr 480
Db      5679 GAGAGAGTCTGTGCTGCTGATGATGACAAAGCCCACTCTGTGATGATGACCTCACCC 5738
Qy      481  ThrTrrGlnLeuCysAlaArgTrrPheCysGlyValIleProSerProLeuArgAspMetPhe 500
Db      5739 ACCTACAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5798
Qy      501  ProValArgProLeuAspThrGlnProProAlaAlaSerHisThrAlaAsnProIleVal 520
Db      5799 CCGTGTGGGCTTGTGACACGGAACCCCGGACAGCCACAGGCAACCCAAAGGTG 5858
Qy      521  ProGlnGlyAspSerIleAlaAspValSerIleMetTrrSerGlnGlnLeuGlyIleGln 540
Db      5859 CCTGAGGGGACTCCATCGCGGAGCTGAGCATCATGACAGTGAAGAGCTGGGACAGCAG 5918
Qy      541  IleLeuIleHisGlnGlnIleSerLeuTrrPheTrrCysSerMetSerSerTrrSerSerSer 560
Db      5919 ATCTGATTCACACAGAACTCATCTGACTGCTCATGCTCTCTCTCTCTCTCTCTCTCTCT 5978
Qy      561  ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer 580
Db      5979 CCAACCCCGCCAGGCTGCGCAAGTCCCTTCAAGCTCCCAAGCTCCCAAGCAATTTCTTC 6038
Qy      581  SerValProPheSerTrrPheCysGlyAspSerAspMetLeuHisThrProGlyAlaAla 600
Db      6039 AGTGTGCTTCTTCTCACCGCACTGTGAGAGCTCAGACATGCTAATACGCCGCTGTCTCC 6098
Qy      601  SerAspArgSerGlnHisAspLeuTrrPheMetAspGlyGlnTrrPheSerGlnHisLeu 620
Db      6099 TCCGACAGCTGTGACATGACCTGACCCCAATGACCGGAGACCTTACCGACGACCTG 6158
Qy      621  GlnAlaValIleIleLeuAlaValArgAspLeuIleTrrValIleProArgArgIleGlyAsp 640
Db      6159 CAGGCGCGAAGATCTCCGCGCTCAGAGACCTCATTTGGTGTCCCGCCAGCGCGGTGAGAT 6218
Qy      641  ValIleValIleGlyLeuGlnIleAspSerGlnAlaGlnArgGlyArgValIleAlaVal 660
Db      6219 GTTATGCTATGCTGCTGAGAGAGATTTCTGGCGCCCAAGCGGGGCCGACATTCGCCCTC 6278
Qy      661  LeuIleValIleArgGlnLeuTrrProHisGlyValIleValIleAspAlaAlaValAlaIle 680
Db      6279 TTAAGAGCCGAGAGCTGACTCCGCAAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6338
Qy      681  AsnThrValValIleCysTrrPheGlnAsnGlnAsnThrGlnTrrCysIleLeuAlaIleTrrArg 700
Db      6339 GACACTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6398
Qy      701  GlyTrrGlyAlaArgGlnPheAspIlePheTrrGlnSerTrrGlnGlnLeuGlyArgLeu 720
Db      6399 GCGTGGGCGCCAGAGAGTTCGATATTTTTCACAGTCTACAGAGGAGCTGGCGCGCTG 6458
Qy      721  GlnAlaCysThrArgIleArgArg 728
Db      6459 GAGGCTTGCACTGCAAGAGAGG 6482

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RESULT 6  
US-10-094-749-50  
Sequence 50. Application US/10094749  
Publication No. US20030219741A1  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TARAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUKIO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOTIKO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOKYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA  
FILE REFERENCE: 08435/0160  
CURRENT APPLICATION NUMBER: US/10/094,749  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/350,435  
PRIOR FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: JP 2001-328381  
PRIOR FILING DATE: 2001-09-14  
NUMBER OF SEQ ID NOS: 3381  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50  
LENGTH: 3112  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-094-749-50

Alignment Scores:  
Pred. No.: 0 Length: 3112  
Score: 3225.00 Matches: 616  
Percent Similarity: 99.84% Conservat: 0  
Best Local Similarity: 99.84% Mismatches: 1  
Query Match: 84.38% Indels: 1  
DB: 13 Gaps: 0

US-09-836-392-21 (1-728) x US-10-094-749-50 (1-3112)

QY 112 VallyeGluHieilleaenilleysleuseAepTYRGIYliSeraGlnSerPheHis 131  
DB 2 GTCAAGAGACATCAACATCAAGCATGTGACTACGGGATTTCAGGCACTTTCAT 61  
QY 132 GlnGlyAlaLeuGlyValGluGlyThrProGlyTYRGINAlaProGlnIleArgProArg 151  
DB 62 GAGGGGCGCTAGCGCTGAGGAGGCACTCTGCTCCAGGCCCGCAGATCAGGCTTCG 121  
QY 152 IleValTYRAspGluTySValAspMetPheSerTYRGIYMetValIleuTYRGIYIleuIleu 171  
DB 122 ATTGTATATGATAGAAAGTAAATATGTTCTCTTATGAAATGCTCTTACAGATTGCTG 181  
QY 172 SerGlyGlnArgProAlaLeuGlyHisHisGlnLeuGlnIleAlaValLeuSerIys 191  
DB 182 TCAGGACAGCGCCCTGCACTGGGCGCACACAGCTCCAGATTGCCAAGAACTGTCCAG 241  
QY 192 GlyIleArgProAlaLeuGlyGlnProGluGluValGlnPheArgArgLeuGlnAlaLeu 211  
DB 242 GGCATCCGCGCGGTCTTGCGGCAAGCGGAGAAAGTGCATTTCCGCGACTGCAAGCGCTC 301  
QY 212 MetMetGlnCySerTrpAspThrIysProGluTySArgProLeuAlaLeuSerValIleSer 231  
DB 302 ATGATGGAGTGCTGGGACACTAGCCAGAGAGCAAGCGCTGCGCTGTGGGTGGTGGC 361  
QY 232 GlnMetIleAspProThrPheAlaThrPheMetTYRGIYIleuCySValGlyIleGlnThr 251  
DB 362 CAGATGAAGACCCGACTTTCGACCTTCATGTATGAACCTGTGCTGGGAAGAGACA 421  
QY 252 AlaPheSerSerSerGlnGlyGlnGlyIleValIlePheTrpAspGlyIleSgIleGln 271  
DB 422 GCCTTCTTCTCATCCAGGCGCAGAGTACACCGTGTGTTTGGGATGGAAAAGAGAG 481  
QY 272 SerArgAsnTYRThrValValAlaThrTrpGluGlyLeuMetGlnValGlnArgMetCys 291  
DB 482 TCCAGGAACCTACAGCGGTGTGAACACAGAGAGGCGCTCATGAGAGTGCAGAGATGTGC 541

QY 292 CySProGlyMetIleValSerCySglnLeuGlnValGlnArgSerIleuTrpThrAlaThr 311  
DB 542 TGCCCTGGAGTGAAGGTGAGGTGCACTCCAGCTCCAGATCCAGATCCCTGTGGAGAGCACCC 601  
QY 312 GlnAspGlnTySleTYRleTYRThrLeuGlyMetCySProLeuAsnThrProGln 331  
DB 602 GAGACCAAGAAATCTACATCTACACCTCAAGGCAATGCGCCCTTAAACACACCCCA 661  
QY 332 GlnAlaLeuAspThrProAlaValIleThrCySPhelLeuAlaValProValIleIleValS 351  
DB 662 CAGGCTTGATCTCCAGGCTGTGTCACTGCTTTCGCGCTGCTGTATTAAAGG 721  
QY 352 AsnSerTYRleuValIleuAlaGlyIleuAlaAspGlyIleuValAlaValPheProValAl 371  
DB 722 AATTCCTACCTGTGCTTACGCGGCTTCGCGGATGCGCTTGTGCTGTTCCTCCGCGTG 781  
QY 372 ArgGlyTYRProTySAspSerCySserTYRleuCySserHisThrAlaAsnArgSerIys 391  
DB 782 CGGGGACCCCAAGAGACAGCTGCTCTTACCTGTGCTCACACACAGCCACAGCTCCAG 841  
QY 392 PheSerIleAlaAspGluAspAlaArgGlnAsnProHyProValIleAlaMetGluVal 411  
DB 842 TTCAGCATCGGAGTGAAGACGACGCGCAAGCCCTACCAAGTGAAGGCCATGAGAGT 901  
QY 412 ValAsnSerGlySerGluValIleTrpTYRserAsnGlyProGlyIleuValIleAspCys 431  
DB 902 GTCAACACGCGCTGAGGTCTGTGTACAGCAAGGCGCGGCTCTGTGCATCGACTGT 961  
QY 432 AlaSerLeuGlnIleCYAArgArgLeuGluProTYRMetAlaProSerMetValIleSer 451  
DB 962 GCGTCCCGGAGATCTGAGGCGGCTGAGCCCTACATGCCCCCTTCATAGTGTAGTCA 1021  
QY 452 ValValCySserSerGlnGlyArgGlyGluValValIleProCySleuAspAlaVal 471  
DB 1022 GTGCTGTCACTCTGAGCGGACAGGAGGAGAGGTCTGTGCTGTGATGACAGAGCC 1081  
QY 472 AsnSerLeuValMetTYRHisSerThrTYRglnLeuCySAlaArgTYRPhCYGly 491  
DB 1082 AACTCCTGTGATGATACCACTCCACCACTACCACTGCTGTGCGCGTACTTCTCGGG 1141  
QY 492 ValProSerProLeuArgAspMetPheProValArgProLeuAspTrpGluProProAla 511  
DB 1142 GTCCCAAGCCCCCTCAGGACATATTTCCGTGGGCGCTTGGACACAGAACCCCGGCA 1201  
QY 512 AlaSerHisThrAlaAsnProValProGluGlyAspSerIleAlaAspValSerIle 531  
DB 1202 GCCAGCCACACGGCCCAACCAAGGTGCTGAGGGGAGCTCCATCGCGGACGTGAGCATC 1261  
QY 532 MetTYRserGlnGluLeuGlyTYRglnIleIleuIleHisGlnIleuSerLeuThrAspTYR 551  
DB 1262 ATGTACAGTGAAGAGCTGGGACAGAGATCTGTATCCACAGAAATACCTCATGACTAC 1321  
QY 552 CySserMetSerSerTYRserSerSerProProArgIleAlaIleArgSerProSerSer 571  
DB 1322 TGCTCCATGTCTCTTACTCTCATCCCAACCCGCGAGGCTGCAGATGCCCTCAAGC 1381  
QY 572 LeuProSerSerProAlaSerSerSerSerValProPheSerThrAspCySValAspSer 591  
DB 1382 CTCCCAACTCCCAAGAGTCTTCCAGTGTGCTTCTCCACGCACTCGAGAGACTCA 1441  
QY 592 AspMetLeuHisThrProGlyAlaAlaSerAspArgSerGlnHisAspLeuThrProMet 611  
DB 1442 GACATGTCTACATAGCCCGGTGCTGCTCCGACAGAGCTGAGCATGATGACCCCATG 1501  
QY 612 AspGlyGlnThrPheSerGlnHisLeuGlnAlaValIleIleuAlaValArgAspLeu 631  
DB 1502 GACGGGAGACCTTGAAGCACACCTGAGGCGCTGAGAGATCTGCGCTCAGAGACTC 1561  
QY 632 IleTrpValProArgArgGlyIleAspValIleValIleGlyLeuGlnTySAspSerGln 651  
DB 1562 ATTTGGGTCCCAAGCGCGT-GAAGATTTATCTCATTTGGCCTGGAAGAGATTCGA 1620



Pred. No.: 4,91e-27 Length: 3052  
 Score: 341.50 Matches: 111  
 Percent Similarity: 48.35% Conservative: 80  
 Best Local Similarity: 28.10% Mismatches: 150  
 Query Match: 8.94% Indels: 55  
 DB: 13 Gaps: 14

US-09-836-392-21 (1-728) x US-10-115-482-47 (1-3052)

QY 10 Alamelysanpserglu-----Phearginglualeasermet 23  
 DB 999 GCTGTGAAGATTTTAAATAACATACACTCAGGCTGTAGACAGAGCTGTGGTG 1058  
 QY 24 LeuhsalaleuGlnHisProCysIleValAlaLeuilegylIleSerIleHisProleu 43  
 DB 1059 CTTTGCCACCTCCACCCACCCAGTTTATCTTGCTGGAGCTGGAGTTCTGCCCCG 1118  
 QY 44 CysPheAlaleuGluLeuAlaProleuserSerleuAnthrValleuserGluAnala 63  
 DB 1119 ATGTTGGTATGAGATTTAGCTCCAGAGGTTCTTGATGCGCTTCACGACAGCAAA 1178  
 QY 64 ArgasPserSerPheIleProleuGlyHisMetleuThrGlnIleAlaTyrglnIle 83  
 DB 1179 GCACG-----CTCACTGAACCTCAGACAGAGATTGGACTCCAGCTA 1223  
 QY 84 AlaSerGlyLeuAlaTyrlleuHisIleIleValAsnIleIlePheCysAspLeuIleSerAsp 103  
 DB 1224 GCTGATGTTGATGATCTCCACCTCCAGCCATGATATATATACAGAGCTGAAACCCAC 1283  
 QY 104 AsnIleLeuValIlePheSerleuAspValIleGlnHisIleAsnIleIleLeuSerAspTy 123  
 DB 1284 AATGTGCGCTTTTACACTGATGCCAATGCCATGCTGCAATGCAAGATTGCTGACTAC 1343  
 QY 124 GlyIleSerArgIleSerPheHisIleGlnIleValIleGlnIleGlnIleThrProGlyTy 143  
 DB 1344 GGCATTTGCTCACTGCTGTAGAAATGGGATTAATAACATCAGAGGACACACAGGATTT 1403  
 QY 144 GlnAlaProGluIle---ArgProArgIleValTyrlasGlnIleValIleAspMetPheSer 162  
 DB 1404 CGTGACCTCGAAGTTCAGAGAGAAATGCTATTTATACCAACAGGCTGATGTTATCA 1463  
 QY 163 TyrglyMetValleuTyrgluLeuLeu---SerGlyIleArgProAlaLeuGly----- 179  
 DB 1464 TTGGTTTACTACTGATGACATTTTGCAACTGAGGTAAATAGTAGAGGTTTGAAAG 1523  
 QY 180 -----HisIleGlnleuGlnIleAlaIleIleValIleSerIleGlyIleArgPro 195  
 DB 1524 TTTCGAATGAGTTGATGATTAATTAACAGAAATTAATCTGATCCAGTTAAAGAA 1583  
 QY 196 ValIleuGlnProGlnIleValIleGlnPheArgIleGlnAlaIleuMetMetGluCys 215  
 DB 1584 TATGTTGTGCCCA-----TGGCCTATGTTGAGAATTAATAACAGTGT 1631  
 QY 216 TrpAspThrIleProGlnIleArgProleuAlaIleuSerValIleSerGlnMetIleAsp 235  
 DB 1632 TTGAAGAAATCCCAAGAAAGGCTTCTCTGCCAGGATTTCTCTCAGGCTTTGAC 1691  
 QY 236 ProThrPheAlaThrPheMetTyrgluLeuCysCysGlyIleGlnIleAlaPhe----- 253  
 DB 1692 ATTTGAATTCAGCT-----GATTAAGTCTGTCT-GACGAGAGAGCAATTTATTAAC 1741  
 QY 254 -----PheSerSerGlnIleGlnIle-----Tyr 261  
 DB 1742 TAAAAAGTAAATGTTGAATGATGATGTTGCTACATACATACAGACAGCAATGCAAGAT 1801  
 QY 262 ThrValIlePheTrpAspGlyIleGlnIleSerArg-AsnTyrlleValIleAnthrGln 281  
 DB 1802 TTGGCTGGGCTGTGGGACACCGACAGAGAGAGAGCTCTCATTTCTTGACTTAATATCGA 1861  
 QY 281 ulysGlyIleuMetGluVal-----GlnArgMetCysCysProGlyMetIleValse 298  
 DB 1862 AGGATACACTTCTGAGAGAGTGTGATAGTATGATATGTTGCTTACGCTTG----- 1913

QY 298 rCysGlnleuGlnValGlnArgSerleuTrp-----ThrAlaThrGlnAspGlnIle 316  
 DB 1914 -GTGCATCTTCCTGTGAAAGAAAGAGCTGATGTTGCTGGACACAGTCTGTACTCT 1972  
 QY 316 eTyrlleTyrlleuGlyMetCysProleuAnthrProGlnGlnAlaIleuAspTh 336  
 DB 1973 CCGTGATCAATACCGAAGATGGGAAAAAGACATACCTACAGAAAGATGACTGATTC 2032  
 QY 336 rProAlaValIleThrCysPheleuAlaValProValIleIle-----LysAsnSerTy 354  
 DB 2033 T-----GTCACTGTTGTTGATTGCAATTCCTTTCCAGCAAGCAACAAAAA 2083  
 QY 354 rLeuValleuAlaGlyLeuAlaAspGlyLeuValAlaValAlaPhe 368  
 DB 2084 TTTTCTTTGTTGGTGAACCGCTGATGCAAGTTAGCAATTTT 2126

RESULT 9  
 US-10-115-482-49  
 / Sequence 49, Application US/10115482  
 / Publication No. US20030212257A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Syntek, et al.  
 / TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM  
 / TITLE OF INVENTION: AND METHODS  
 / TITLE OF INVENTION: OF USING THE SAME  
 / FILE REFERENCE: 21404-322D  
 / CURRENT APPLICATION NUMBER: us/10/115,482  
 / CURRENT FILING DATE: 2002-04-05  
 / PRIOR APPLICATION NUMBER: 60/281,086  
 / PRIOR FILING DATE: 2001-04-03  
 / PRIOR APPLICATION NUMBER: 60/281,136  
 / PRIOR FILING DATE: 2001-04-03  
 / PRIOR APPLICATION NUMBER: 60/281,863  
 / PRIOR FILING DATE: 2001-04-05  
 / PRIOR APPLICATION NUMBER: 60/281,906  
 / PRIOR FILING DATE: 2001-04-05  
 / PRIOR APPLICATION NUMBER: 60/282,534  
 / PRIOR FILING DATE: 2001-04-10  
 / PRIOR APPLICATION NUMBER: 60/283,512  
 / PRIOR FILING DATE: 2001-04-12  
 / PRIOR APPLICATION NUMBER: 60/285,325  
 / PRIOR FILING DATE: 2001-04-19  
 / PRIOR APPLICATION NUMBER: 60/285,890  
 / PRIOR FILING DATE: 2001-04-23  
 / PRIOR APPLICATION NUMBER: 60/286,068  
 / PRIOR FILING DATE: 2001-04-24  
 / PRIOR APPLICATION NUMBER: 60/286,292  
 / PRIOR FILING DATE: 2001-04-25  
 / PRIOR APPLICATION NUMBER: 60/287,213  
 / PRIOR FILING DATE: 2001-04-27  
 / PRIOR APPLICATION NUMBER: 60/288,257  
 / PRIOR FILING DATE: 2001-05-02  
 / PRIOR APPLICATION NUMBER: 60/291,134  
 / PRIOR FILING DATE: 2001-05-15  
 / PRIOR APPLICATION NUMBER: 60/282,020  
 / PRIOR FILING DATE: 2001-04-06  
 / PRIOR APPLICATION NUMBER: 60/291,725  
 / PRIOR FILING DATE: 2001-05-17  
 / PRIOR APPLICATION NUMBER: 60/294,771  
 / PRIOR FILING DATE: 2001-05-31  
 / PRIOR APPLICATION NUMBER: 60/296,965  
 / PRIOR FILING DATE: 2001-06-08  
 / PRIOR APPLICATION NUMBER: 60/299,128  
 / PRIOR FILING DATE: 2001-06-08  
 / NUMBER OF SEQ ID NOS: 149  
 / SEQ ID NO 49  
 / LENGTH: 3040  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE: CDS  
 / NAME/KEY: (108), (2841)  
 / LOCATION: (108)  
 US-10-115-482-49

## Alignment Scores:

Pred. No.: 8,2e-26 Length: 3040  
 Score: 330.50 Matches: 108  
 Percent Similarity: 47.34% Conservative: 79  
 Best Local Similarity: 27.34% Mismatches: 150  
 Query Match: 8.65% Indels: 59  
 DB: 13 Gaps: 14

US-09-836-392-21 (1-728) x US-10-115-482-49 (1-3040)

QY 10 AlameltyAsnPheserGlu-----PheArgGlnGluAlaSerMet 23  
 DB 999 GCTGTGAAGATTATTAATTAACATACATCACTCAGGCTGTATTAACAAGAGCTGTGGTG 1058  
 QY 24 LeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHisProLeu 43  
 DB 1059 CTTTGGCACCCTCCACCACCCCGATTGATCTTTGGCTGGCAGCTGGAGATTCTCCCGG 1118  
 QY 44 CysPheAlaLeuGlnLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla 63  
 DB 1119 ATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1178  
 QY 64 ArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnIleAlaTyrglnIle 83  
 DB 1179 GCCAGC-----CTCCTAGAACCTTACAGCAGCAGAGATTGACCTCCAGTA 1223  
 QY 84 AlaSerGlyLeuAlaTyrlleuHisIleCysAsnIleIlePheCysAspLeuIleSerAsp 103  
 DB 1224 GCTGATGCTTTAGATACCTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 1283  
 QY 104 AsnIleLeuValTrpSerIleAspValIleGlyIleHisIleAsnIleIleSerAspTy 123  
 DB 1284 AATGTGCTCTTTTACACCTGATCCCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATG 1343  
 QY 124 GlyIleSerArgGlnSerPheHisGlnIleValAlaLeuGlyValIleGlyIleProGly 143  
 DB 1344 GGCATTGCTCAGTACTGCTGTAAGATGGGATTAATAAATCAGAGGGGACACACAGGGTTT 1403  
 QY 144 GlnAlaProGlnIle---ArgProArgIleValTyraProGlyValIleSerMetPheSer 162  
 DB 1404 CGTGACCTGAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463  
 QY 163 TyrglyMetValLeuTyrglyLeuLeu---SerGlyIleArgProAlaLeuGly----- 179  
 DB 1464 TTTGGTTTACTACTATGACATTTTGACAACTGAGGTAGAAATAGTAGAGGGTTTGAAG 1523  
 QY 180 -----HisIleGlnLeuGlnIleAlaIleValIleSerIleSerIleGlyIleArgPro 195  
 DB 1524 TTTCCAATGAGTTGATGATTAAGAAATACAGAGAAATTAATCACTTCCAGTTAAAGAA 1583  
 QY 196 ValLeuGlyGlnProGlyGlnIleValGlnPheArgIleGlnAlaLeuMetMetGluCys 215  
 DB 1584 TATGTGTGGCCCA-----TGGCCTATGGTTGAAAATTAATTAATAAAGACTGT 1631  
 QY 216 TrpAspThrValProGlyIleArgProLeuAlaLeuSerValIleSerGlnMetIleAsp 235  
 DB 1632 TTGAAGAAATATCCCAAGAAAGGCTTCTCTGCCAGGCTTGTGACATTTTAATTC 1691  
 QY 236 ProThrPheAlaThrPheMetTyrglyLeuLeuCysGlyIleGlnIleAlaPhe----- 253  
 DB 1692 GCT-----GAATTAAGTCTCTC-GAGCAGAGAGCATTTTATTAC 1729  
 QY 254 -----PheSerSerGlnIleGlnIle-----Tyr 261  
 DB 1730 TAAAAACGTAATGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1789  
 QY 262 ThrValAlaPheTrpAspGlyValGlnIleSerArg---AsnTyrlleValAlaLeuThrG 281  
 DB 1790 TTGGCTGGGCTGTGGGACACCGACAGAGACAGCTCATTTCTTGAATTAATTAATTCGA 1849  
 QY 281 ulysGlyLeuMetGluVal-----GlnArgMetCysCysProGlyMetIleValSe 298

DB 1850 AGGATACACTTCTGAGGAAGTTGCTGATGATGATGATGATGATGATGATGATGATGATG 1901  
 QY 298 rCysGlnLeuGlnValGlnArgSerLeuTrp-----ThrAlaThrGlnAspGlnIle 316  
 DB 1902 -GTGCATTTCTCTTTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1960  
 QY 316 eTyrlleTyrlleThrLeuIleGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAsp 336  
 DB 1961 CTTGTCTCAATATCCGAAATGCGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2020  
 QY 336 rProAlaValAlaThrCysPheLeuAlaValProValIleIle-----LysAsnSerTy 354  
 DB 2021 T-----GTCACTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2071  
 QY 354 rLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPhe 368  
 DB 2072 TTTTCTTTTGTGTGAAACCGCTGATGAGCAAGTTATGACATTTT 2114  
 RESULT 10  
 US-10-335-687A-3  
 / Sequence 3, Application US/10335687A  
 / Publication No. US20030166222A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Meyers, Rachel E.  
 / TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.  
 / TITLE OF INVENTION: 39267, Human Kinase Family Members and  
 / FILE REFERENCE: MP102-001PIRNM  
 / CURRENT FILING DATE: 2003-01-02  
 / PRIOR APPLICATION NUMBER: 60/345,773  
 / NUMBER OF SEQ ID NOS: 20  
 / SOFTWARE: FASTSEQ for Windows Version 4.0  
 / SEQ ID NO 3  
 / LENGTH: 5457  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: (1)...(5457)  
 US-10-335-687A-3  
 Alignment Scores:  
 Pred. No.: 2.08e-25 Length: 5457  
 Score: 330.50 Matches: 108  
 Percent Similarity: 47.34% Conservative: 79  
 Best Local Similarity: 27.34% Mismatches: 150  
 Query Match: 8.65% Indels: 59  
 DB: 13 Gaps: 14  
 US-09-836-392-21 (1-728) x US-10-335-687A-3 (1-5457)  
 QY 10 AlameltyAsnPheserGlu-----PheArgGlnGluAlaSerMet 23  
 DB 3601 GCTGTGAAGATTATTAATTAACATACATCACTCAGGCTGTATTAACAAGAGCTGTGGTG 3660  
 QY 24 LeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHisProLeu 43  
 DB 3661 CTTTGGCACCCTCCACCACCCCGATTGATCTTTGGCTGGCAGCTGGAGATTCTCCCGG 3720  
 QY 44 CysPheAlaLeuGlnLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla 63  
 DB 3721 ATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3780  
 QY 64 ArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnIleAlaTyrglnIle 83  
 DB 3781 GCCAGC-----CTCCTAGAACCTTACAGCAGCAGAGATTGACCTCCAGTA 3825  
 QY 84 AlaSerGlyLeuAlaTyrlleuHisIleCysAsnIleIlePheCysAspLeuIleSerAsp 103  
 DB 3826 GCTGATGCTTTAGATACCTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 3885

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QY 104 AsnIleLeuValTTPSeLeuAspValIysGluHisIleAsnIleYLeuSerAspTyr 123
DB 3886 AATGCTGCTTTTACACTGTATCCCATCTCCATCTCATCTTGCAGAAAGATGCTGCTAC 3945
QY 124 GlyIleSerArgInserPheHisGluGlyAlaLeuGlyValGluGlyTyrProGlyTyr 143
DB 3946 GGCATTGCTCAGTACTGCTGTAGAAATGGGGATAAACATCAGAGGACACACAGGCTTT 4005
QY 144 GlnAlaProGluIle---ArgProArgIleValTyrAspGluYsValAspMetPheSer 162
DB 4006 CGTGACCTGAAGTTGGCCAGAGAAATGCTATTATACCAACAGCGCTGATTATATCA 4065
QY 163 TyrGlyMetValLeuTyrGluLeuLeu---SerGlyGlnArgProAlaLeuGly----- 179
DB 4066 TTGGTTTACTACTATGACATTTTGCAACTGAGAGGTAGAAATAGTAGAGGGGTTGAAG 4125
QY 180 -----HisHisGlnLeuGlnIleAlaIleAlaYsLeuSerIysGlyIleArgPro 195
DB 4126 TTCCAAATGAGTTGATGATGATTAAGAAATACAGAGAAATTAACCTGATCCAGTTAAAGAA 4185
QY 196 ValLeuGlyGlnProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCys 215
DB 4186 TATGTTGTGCCCA-----TGCCCTATGTTGAGAAATTAATTAACAGTGT 4233
QY 216 TTPAspThrLysProGluLysArgProLeuAlaLeuSerValIleSerGlnMetLysAsp 235
DB 4234 TTGAAGAAATCCCTCAGAAAGGCTTCTGCCCCAGCTTTGACATTTGAATTC 4293
QY 236 ProThrPheAlaThrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhe----- 253
DB 4294 GCT-----GAAATGATCTGTCT-GACGAGAGCATTTTATTATACC 4331
QY 254 -----PheSerSerGlnGlyGlnIle-----Tyr 261
DB 4332 TAAAAACGTAATTTGTAATGCATGCTGCTACATACATACACAGCAGAAAGCAAGAT 4391
QY 262 ThrValAlaPheTyrAspGlyLysGluLeuSerArg-AsnTyrThrValAlaLeuThrGln 281
DB 4392 TTGGCTGGGCTGTGGGACACCCAGACAGACAGCTCATTTTGTGACTTAATACTGA 4451
QY 281 IlySerGlyLeuMetGluVal-----GlnArgMetCysSerProGlyMetLysValSe 298
DB 4452 AGGATACACTTCTGAGAAAGTTGCTGATAGTAAGTAATGCTTACCTTG----- 4503
QY 298 rCysGlnLeuGlnValGlnArgSerLeuTyr-----ThrAlaThrGlnAspGlnIle 316
DB 4504 -GTGCATCTTCCGTGAAAGAAAGAGAGTGTGTGTCTGTGGACACAGCTGTACTCT 4562
QY 316 eTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThr 336
DB 4563 CCTGTCATCAATACCGAAGATGGAAAAAGAGACATACCTTGAAGAAAGTACTGATTC 4622
QY 336 rProAlaValAlaThrCysPheLeuAlaValProValIleLys-----LysAsnSerTyr 354
DB 4623 T-----GTCACTGTTTGTATTTGCAATTCCTTTCCAAAGCAAGCAAAACAAAAA 4673
QY 354 rLeuValIleuAlaGlyLeuAlaAspGlyLeuValAlaValPhe 368
DB 4674 TTTTCTTTGTTGTTGAACCGCTGATGCGAAGTTACCAATTTT 4716

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## RESULT 11

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US-10-335-687A-6
Sequence 6, Application US/10335687A
Publication No. US20030166222A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 39267, Human Kinase Family Members and
FILE REFERENCE: MP102-001PRM
CURRENT APPLICATION NUMBER: US/10/335,687A
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: 60/345,773

```

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PRIOR FILING DATE: 2002-01-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 5475
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(5475)
US-10-335-687A-6

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## Alignment Scores:

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Pred. No.: 2,09e-25 Length: 5475
Score: 330.50 Matches: 108
Percent Similarity: 47.34% Conservative: 79
Best Local Similarity: 27.34% Mismatches: 150
Query Match: 8.65% Indels: 59
DB: 13 Gaps: 14

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US-09-836-392-21 (1-728) x US-10-335-687A-6 (1-5475)

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QY 10 AlavetLysAsnPheSerGlu-----PheArgGlnGluAlaSerMet 23
DB 3601 GCTGTGAAGATTTTATTAATAAATACATCACTCAGCGCTGTAAGACAGAGCTTGCTG 3660
QY 24 LeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHisProLeu 43
DB 3661 CTTTGCACCTCCACACCCAGTTTATATCTTTGCTGGACAGCTGGATTCCTCCCG 3720
QY 44 CysPheAlaLeuGlnIleuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla 63
DB 3721 ATGTTGGATGAGAGTTAGCTCAGGCTCCAGAGGTTCTTGATGCGCTGCTCAGCAGCAAA 3780
QY 64 ArgAspSerSerPheIleProLeuGlnHisMetLeuThrGlnIleAlaTyrGlnIle 83
DB 3781 GCCAGC-----CTACTAGAACCTTACAGACAGAGTTGCTCCACGTA 3825
QY 84 AlaSerGlyLeuAlaTyrLeuHisIlyLysAsnIleIlePheCysAspLeuLysSerAsp 103
DB 3826 GCTGATGTTTGAATATCTCCATCAGCACTGATATTAATACCGAAGCTGAAACCCAC 3885
QY 104 AsnIleLeuValTTPSeLeuAspValIysGluHisIleAsnIleYLeuSerAspTyr 123
DB 3886 AATGCTGCTTTTACACTGTATCCCATCTCCATCTCATCTTGCAGAAAGATGCTGCTAC 3945
QY 124 GlyIleSerArgInserPheHisGluGlyAlaLeuGlyValGluGlyTyrProGlyTyr 143
DB 3946 GGCATTGCTCAGTACTGCTGTAGAAATGGGGATAAACATCAGAGGACACACAGGCTTT 4005
QY 144 GlnAlaProGluIle---ArgProArgIleValTyrAspGluYsValAspMetPheSer 162
DB 4006 CGTGACCTGAAGTTGGCCAGAGAAATGCTATTATACCAACAGCGCTGATTATATCA 4065
QY 163 TyrGlyMetValLeuTyrGluLeuLeu---SerGlyGlnArgProAlaLeuGly----- 179
DB 4066 TTGGTTTACTACTATGACATTTTGCAACTGAGAGGTAGAAATAGTAGAGGGGTTGAAG 4125
QY 180 -----HisHisGlnLeuGlnIleAlaIleAlaYsLeuSerIysGlyIleArgPro 195
DB 4126 TTCCAAATGAGTTGATGATGATTAAGAAATACAGAGAAATTAACCTGATCCAGTTAAAGAA 4185
QY 196 ValLeuGlyGlnProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCys 215
DB 4186 TATGTTGTGCCCA-----TGCCCTATGTTGAGAAATTAATTAACAGTGT 4233
QY 216 TTPAspThrLysProGluLysArgProLeuAlaLeuSerValIleSerGlnMetLysAsp 235
DB 4234 TTGAAGAAATCCCTCAGAAAGGCTTCTGCCCCAGCTTTTGAATTTGAATTC 4293
QY 236 ProThrPheAlaThrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhe----- 253
DB 4294 GCT-----GAAATGATCTGTCT-GACGAGAGCATTTTATTATACC 4331

```





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19  GlnGluAlaSerMetLeuHisnAlaLeuGlnHisProCysIleValAlaLeuIleGlyLe 38
718 CAGGAAGCCCGGCTCTTTGGAGCCCTTGAGACCCACACATAATGGCCCTTAGGGGGCC 777
39  SerIleHisPro-----LeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsn 56
778 TGCCCTCAACCCCAACACCTCTGCTAGTATGAGATGCGCGGGGTGTGACTGAGC 837
57  ThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGlyHisMetLeuThr 76
838 AGGGTGTCTGGCAGGTGCGCGG-----GTGCCA---CCTCAGTGTGTGTC 879
77  GlnLysIleAlaTyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLys----- 93
880 ---AACTGGGCTGTGAGTGGCGCGGGGATGACTACCTACCAATGATGCCCTGTG 936
94  AsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTrpSerLeuAspValLys 113
937 CCCATCATCCACCGGAGCTCAAGTCCATCACTCCTGATC-----CTGGAGGCCATC 990
114 GluHisIleAsn-----IleLysLeuSerAspTyrGlyIleSerArgGln 128
991 GGAACCAACALCCTCGACAGACGGGTGCTCAAGATCACGGACTTCGGCCCTCGCCCGAG 1050
129 SerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIle 148
1051 TGGCAACAAGACCACCAAGATGAGCGTGGCGGACCTACCGCTGGATGGCGCGGAGTT 1110
149 ArgProArgIleValTyrAspGluLysValAspMetPheSerTyrGlyMetValLeuTyr 168
1111 ATCCGTCTCTCCCTCTCTCCAAAGACAGTATGCTCTGGAGCTTCGGGGTGTCTGTGG 1170
169 GluLeuLeuSerGlyGlnArgProAlaLeuGlyHisIleGlnLeuGlnIleAla----- 186
1171 GAGTGTCTGACGGGGAGTCCCTACCGTGAATGCACCCCTTGCCCGTGGGCTATGGC 1230
187 -----LysLysLeuSerLysGlyIleArgProValLeuGlyGlnProGluGluVal 203
1231 GTGGCTATGAATAAGCTGACGCTGCCATTCCTCCACGTGCCCGAGGCC----- 1281
204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg 223
1282 ---TTTGCCGC-----CTCTCGAGAAATGCTGGGACCCACACCCCGCGGGCGG 1329
224 ProLeuAlaLeuSerValSerGlnMetLysAspProThrPheAlaThrPheMetTyr 243
1330 -----CCAGATTTCGTAGCATCTTGAG 1353
244 GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnTyrThrVal 263
1354 CGGCTGTAAGTATCGAACAGTCAAGCCCTGTTCCAGATGCCACTGGAGTCTTCCACTCG 1413
264 ValPheTrpAspGlyLysGluGluSerArgAsnTyr-----ThrValAlaAsnThrGlu 281
1414 CTGCAGGAAGACTGGAAGCTGAGATTCAACACATGTTTATGACCTTCGGACCAAGAG 1473
282 LysGlyLeuMetGlu-ValGlnArgMetCysCys-----ProGlyLe 295
1474 AAGGAGTTCGGAGCCGTGAGAGAGACTCTCGGGCGGCACAGAGCAGCGCTTCCAG 1533
295 tLysValSerCys-----GlnLeuGlnValGlnArgSerLeuTrpThrAlaThrGln 312
1534 GAGAGAGCTTCGGCGGGGAGCAGGAGCTGGCAGAACGTGAGATGGACA----- 1585
312 uAspGlnLysIleTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGln 332
1586 -----TCGTGGAACGGGAGCTGCACCTGCTCATGTGCCAGCTG 1623
332 nAlaLeuAspThrPro----- 337
1624 AGCCAGGAGAAGCCCGGGTCCGAAAGCGCAAGGGCAACTTCAAGCGCAGCGCGCTGCTC 1683
338 -----AlaValValThrCysPheLeuAlaValProValIleLysLys 351
1684 AAGCTGCGGGAAGCGCGCAGCATCAGCTGCTGCTCTGCTTTGAGCATAGATCACA 1743
351 sAsnSerTyrIleuValValAlaGlyLeuAlaAspGlyLeuValAlaValPhePro----- 369
1744 GTCCAGGCTCTCCAACTCTG-GATAAGCGGAAGATCCGATGGGGCCAGCCCCCTGTC 1802
370 -----ValValArgGlyThrProLysAspSerCysSe 380
1803 AAGCCCGAGCATATCCCCGGCTGAGGGCCATTGCTGACTCCCGTGGAC----- 1854
380 rTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaAr 400
1855 -----TGTGTGGCAGCAGCATGTCACAGCAGTGGAGGAAGTGGGACATGGAGCGC 1907
400 gGlnAsnProTyrProValLys----- 407
1908 CGTGGGCCC-----CCAAAGAGGAGNACTGTGCGGGGCAAGAAGGGAGCAACGTG 1964
408 -----AlaMetGluValVa 412
1965 GGGCCCGCAGCTCCACCTGCGAAGAGGCGGTGGGAGGAGGAGGCTGAAGGGGCT 2024
412 lAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeu----- 426
2025 GGGGAAGGAAGAAACAGTGTCAATGTCGCCCAACCTGGGCAAGTCCCCCAACA 2084
427 -----LeuValIleAspCysAlaSerLeuGluIleCysArgArgLeu----- 440
2085 CACACCATCGCCCTGGCTTCGCCAGCTCAATGATGAGAGGAGTTCGCGGAGGCAGA 2144
441 -----GluProTyrMetAlaProSerMetValThrSerVa 452
2145 GGATGGAGGCGAGCGGTGCCCCCTTCCCTTCTACTCGACCCGCTCTACTCTCAGTGC 2204
452 lValSerSerGluGlyArgGlyGluGluValTrpCysLeuAspAspLysAlaAs 472
2205 ACTGCTCGCGAGCCCTCCCGGGGCGCGGGCGCGTGGAGCGCAGCGCCCTCGCGCC 2264
472 nSerLeuValMetTyrHisSerThrThrTyrGlnLeu-----CysAl 486
2265 CCCCCTGCTGGTGGGACACGCGCGCGCGGCGCTCGACCTGGCGCTGCTAGGCTGCGC 2324
486 a----- 486
2325 CACGCTCTGGGGCTGTGGGCTGGGCCCGCAGCTGGCCGAGGCGCGCGCGCGCAGCG 2384
487 -----ArgTyrPheCysGlyValProSerProLeuArgAspMetPheProVa 502
2385 TGAGGAGCAGCGCGCTGCTCGACGCGCTCTTCTCCCGCGCGCGCGCTTCCCG-- 2442
502 lArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGln 522
2443 -CGGGGCTC-----AGCCCAACCGCGCTCCCCCAGCGCGCGCGCGAGACGTGGGCC 2495
522 uGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGlnIleLe 542
2496 CGGCTGGGCTGGCGCC-----TCGGCCACCCCT 2525
542 uIleHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProPr 562
2526 CGTGTGCTGTGCTGCTGCTGCTGCAACTCCACGCTTCACTGCTGCTGCTGACAG 2585
562 oArgGlnAlaAla-----ArgSerProSerSerLeuProSerProAlaSerSerSe 581
2586 TGACGAGGCGCAGCGCGCGCTCCCCACACCTCCCCCGCGCGCGCCACACCCAC 2645
581 rValProPheSerThr-----AspCysGluAspSerAspMetLeuHisThrPr 597
2646 GCCTCGCCAGACCAACCCCTGCTGGACCTGAGTGGAGCTTCAAGAAGGAGGCC 2705
597 oGly-----AlaAlaSerAspArgSerGluHi 606

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2706 CGGCGAGTGTGTCAGCCGCCACCCACGTCACGGCTGTATGCGTGTGAGCGCGGG---CA 2762

606 sAspLeuThrProMetAspGly 613

2763 CCGGCGGAGCCATCGGATGG 2784

LT 15

0-171-581-312  
quence 312, Application US/10171581  
blication No. US20030104426A1  
NERAL INFORMATION:  
PLICANT: Dai, Hongyue  
PLICANT: Linsley, Peter  
PLICANT: Mao Mao

ITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia

FILE REFERENCE: 9301-157-999

URRENT APPLICATION NUMBER: US/10/171,581

URRENT FILING DATE: 2002-06-14

RIOR APPLICATION NUMBER: 60/298,914

RIOR FILING DATE: 2001-06-18

UMBER OF SEQ ID NOS: 366

Q ID NO 312

LENGTH: 3454

TYPE: DNA

ORGANISM: Homo sapiens

URLICATION INFORMATION:

DATABASE ACCESSION NUMBER: X90846

DATABASE ENTRY DATE: 2001-06-18

0-171-581-312

ment Scores:

. No.: 3,686-23 Length: 3454

e.: 307.50 Matches: 178

ent Similarity: 35.43% Conservative: 87

Local Similarity: 23.80% Mismatches: 272

y Match: 8.05% Indels: 212

15 Gaps: 31

9-836-392-21 (1-728) x US-10-171-581-312 (1-3454)

19 GlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIle 38

718 CAGGAAGCGCGGCTCTTTGGAGCCCTCGAGCACCACCAATAATTGCCCTTAGGGCGCC 777

39 SerIleHisPro-----LeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsn 56

778 TGCCTCAACCCCAACACCTCTGCTAGTGTAGTATGCCCGGGTGTGCTGACTGAGC 837

57 ThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGlyHisMetLeuThr 76

838 AGGGTGTCTGGCAGGTGCGCGG-----GTGCCA---CCTCAGTGTCTGCTC 879

77 GlnLysIleAlaTyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLys----- 93

880 ----ACTGGGCTGTCCAGTGGCCCGGCGGATGATGATGATGATGATGATGATGATGATG 936

94 AsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTrpSerLeuAspValLys 113

937 CCCATCATCCACCGGACCTCAAGTCCATCAACATCCTGATC-----CTGGAGGCCATC 990

114 GluHisIleAsn-----IleLysLeuSerAspTyrGlyIleSerArgGln 128

991 GAGAACCCACACCTCGCAGACAGGTGCTCAAGATCACGACCTTCGGCCCTCGCCCGGAG 1050

129 SerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIle 148

1051 TGGCAACAAGACCAACAGATGAGCGCTCGGGGACCTACGCTGGATGGCGCGGAGTT 1110

149 ArgProArgIleValTyrAspGluLysValAspMetPheSerTyrGlyMetValLeuTyr 168

1111 ATCCGCTCTCCCTCTCTCCAAAGCAGTGTCTGAGCTCGGGGTGCTGCTGG 1170

169 GluLeuLeuSerGlyGlnArgProAlaLeuGlyHisGlnLeuGlnIleAla----- 186

1171 GAGTGTGTCAGCGGCGAGGTCCCTACCTGAGATCGACGCTTGGCGCTGCGTATGCG 1230

187 -----LysLysLeuSerLysGlyIleArgProValLeuGlyGlnProGluGluVal 203

1231 GTGCTATGATTAAGCTGAGCTGCCCATTCCTCCACGTGCCCGAGGCC----- 1281

204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg 223

1282 ---TTTCCCGC-----CTCCTGGAGGAATGTGGGACCCAGACCCACCGGGCGG 1329

224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyr 243

1330 -----CCAGATTTCGTAGCATCTTGAG 1353

244 GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGlyThrVal 263

1354 CGGCTTGAAGTCATCGAACAGTCAGCCCTGTTCCAGATGCCACTGGAGTCTTCCACTCG 1413

264 ValPheTrpAspGlyLysGluGluSerArgAsnTyr-----ThrValValAsnThrGlu 281

1414 CTGAGGAAGACTGGAGCTGAGATTCAGACATGTTTGTGATGACCTTCGGACCAAGGAG 1473

282 LysGlyLeuMetGlu-ValGlnArgMetCysCys-----ProGlyMe 295

1474 AAGAGCTTCGGAGCCGTGAGGAGAGCTGCTGGGGCGGCACAGGAGCAGCGCTTCCAG 1533

295 tLysValSerCys-----GlnLeuGlnValGlnArgSerLeuTrpThrAlaThrGln 312

1534 GAGGACAGCTGCGCGCGGAGCAGGAGCTGGCAGAACGTGAGATGGACA----- 1585

312 uAspGlnLysIleTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGln 332

1586 -----TCGTGGAAACGGAGCTGCACCTGCTCATGTGCCAGCTG 1623

332 nAlaLeuAspThrPro----- 337

1624 AGCCAGGAGAAAGCGCGGGTCCCAAGCGCAAGGGCACTTCAAGCGCAGCGCGCTGTCTC 1683

338 -----AlaValValThrCysPheLeuAlaValProValIleLysLys 351

1684 AAGTGGGGAAGCGGCGGAGCCACATCAGCCTGCCCTTGGCTTTGAGCATAGATCACA 1743

351 sAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPhePro----- 369

1744 GTCCAGGCTCTCCAACTCTG-GATAAGCGGAAAGATCCGATGGGCGCAGCCCTGTC 1802

370 -----ValValArgGlyThrProLysAspSerCysSe 380

1803 AAGCCCGAGCATCATCCCGGCTGAGGGCCATTGCGCTGACTCCCGTGGAC----- 1854

380 rTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaAr 400

1855 -----TGTTGGTGAGCAGCAGTCGCGAGCAGTCAGTGGAGGAAGTGGGACATGGAGCG 1907

400 gLlnAsnProTyrProValLys----- 407

1908 CGTGGGCCC-----CCAAAGAAAGGAAGAACTGTTGCGGGCCAAAGAAAGGGAGCGA 1964

408 -----AlaMetGluValVa 412

1965 GGGGCCCGAGTCCACCTTCAGAGAGCGGGTGGGAGGAGGAGGAGGCTGAGGGGCT 2024

412 lAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeu----- 426

2025 GGGGGAAGGAAGCAACAGTGTGTCATCAAGTCCCGCCCAACCTGGGCAAGTCCCCCAACA 2084

427 -----LeuValIleAspCysAlaSerLeuGluIleCysArgArgLeu----- 440

2085 CACACCATCGCCCTGCTTCCAGCTTCAATGAGTGGAGGAGTTCGCGGAGGCAGA 2144

441 -----GluProTyrMetalProSerMetValThrSerVa 452

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2145 GGATGAGGACAGCAGCTGCGCCCTTCCCTTACTGACACCCCGTCTTACCTCTCAGTGCC 2204
452 lValCysSerSerGluGlyA-gGlyGluGluValValrCysLeuAspAspLysAlaAs 472
   : : : : :
2205 ACTGCTGCGGAGCCCTCCCGGGGCGCGGCGCGCTGGAGCGCGACGCGCTCCGCGCC 2264
472 nSerLeuValMetTyrHisSerThrTyrGlnLeu-----CysAl 486
   : : : : :
2265 CCCCCTCGGTGGGACACAGCGCGCGCGCTGCGACCTGGCGCTGTAGGCTGCGC 2324
486 a----- 486
2325 CACGCTGTGGGGCTGTGGGCTGGGGCGCGACGTGGCGGCGCGCGCGCGCGACGG 2384
487 -----ArgTyrPheCysGlyValProSerProLeuArgAspMetPheProVa 502
   : : : : :
2385 TGAGGAGCAGCGGCGCTGGCTCGACAGCGCTCTTTCGCGCGCGCGCGCTTCCCG-- 2442
502 lArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGl 522
   : : : : :
2443 -CGGGGCTC-----AGCCACCGCGCGTCCCGACGCGCGCGCGAGACGTGGGCC 2495
522 uGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGlnIleLe 542
   : : : : :
2495 CGGCCTGGGCTGGCGCC-----TCGGCCACCT 2525
542 uIleHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerProPr 562
   : : : : :
2526 CGTGTGCTGTGCTCGGTCCGACTGCACTCCACGCTTCACTGTGCGCTCTGACAG 2585
562 oArgGlnAlaAla---ArgSerProSerSerLeuProSerSerProAlaSerSerSerSe 581
   : : : : :
2586 TCACGAGGCGCGACGCGCGCGCTCCCGACCCCTCCCGCGCGCGCGCCACACCCAC 2645
581 rValProPheSerThr-----AspCysGluAspSerAspMetLeuHisThrPr 597
   : : : : :
2646 GCCCTGCGCCAGCACCAACCCCTGTGTGGACCTGGAGCTTCAAGAGGAGCCC 2705
597 oGly-----AlaAlaSerAspArgSerGluHi 606
   : : : : :
2706 CGGCCAGTCGCTACGCCGCCACCCAGTCACGGCTGTATGCGCTGTGAGCGCGGG---CA 2762
606 sAspLeuThrProMetAspGly 613
   : : : : :
2763 CGGGCGGAGCCATCGGATGG 2784
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ch completed: December 14, 2003, 09:04:21  
time : 604 secs



149	CGC-----CGCTCAGCAGCCTCA-----ACACGGTGTCTGTCGAGA	184
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27	ThrThrArgProProAlaAspArgSerGlyAlaThrAlaArgValProAlaCysA-rgAr-g	46
185	ACGCCAGAGATTCTTCCTTTATACCCTCGGACACATGCTCACCCAAAAATAGCTTACC	244
47	Val-----Prolle	49
245	AGATCGCCTCGGCCTGGCTACTGTCACAAGAAAAATCATCATCTTCTGTGACCTGAAGT	304
50	ArgCysAlaAsnAlaTrpPro-----GlyArgProMetSerSerThr-----Ser	64
305	CGGACACATCTTGTTGGTGGCTCAAGAGACACATCAAACATCAAGCTATCTG	364
65	ArgArgProGlyTrpSerProAlaValProAlaGlyAlaCysCysTrpLysThrI-rgAsn	84
365	ACTACGGGATTTCGAGGCAGT-----CATTCCATGAGGGCGCCTTAGCGGTGGAGG	415
85	ValAlaGlyArgSerAlaThrAspAlaTrpSerSerAlaProAlaProAlaAsnCysCys	104
416	GCATCTCTGGCTACCGCCCCAGAGATCAGCCCTCGCATGTATATATGATGACAGAGTAG	475
105	CysLeuPheProAlaGlyProSerProAlaSerProAlaProAlaProAlaCysA-rgAr-g	123
476	ATATGTTCTCTATGGAATGGTGTCTACAGATCTGCTGCAGCAGCGCCCTGCACATGG	535
124	-----TrpProArgAlaAlaCys-----HisTrp	131
536	GCCACCACCGAGCTCCAGATGTCACAAAGACTGTCCAAGGCGATCGCCCGGTCTTGGGCG	595
132	Pro-----AlaSerAlaTrpTrpTrpLeu	139
596	AGCCGGAGGAAGTCAGTTCGCGCAGCTGCAGGCGTCAATGATGGAGTGTGGGACACTA	655
140	AlaProAlaArgCys-----Cys-----	145
656	AGCCAGAGAAGCGACCGCTGGCCCTGTGCGTGGTGAGCCGATGAAGACCCGACTTTTG	715
146	-----TrpProAla-----	148
716	CCACCTTCATGTATGAACGTGTGTGGAGCAGACAGCCTTCTTCTCATCCGAGGCC	775
149	ProProAla-----ProAlaSerAlaGlyA-rgAlaCysCysAlaSerProAsnA-rgAr-g	166
776	AGGAGTACACCGTGGTGTGTTTTGGATGGAAAAGAGAGAGTCCAGGAACCTACACGGTGTGA	835
167	ArgArgGluProTrp-----ProProSerProTyRAlaSerA-rg-----	179
836	ACACAGAAAGGGCCTCATGAGAGTGCAGAGATGTGCTGCCCTGGATGAAGTGAAGCT	895
180	-----AlaGlyProAlaSer-----	184
896	GCCAGCTCCAGGTCCAGATCCCTGTGACAGCCACCCAGGAGCCAGAAAAATCTACATCT	955
195	-----CysGlyA-rgProProAlaCysSerProValAlaThr	196
956	ACACCTTCAAGGCATGTGCCCTTAACACACCCCACACAGGCGCTTGGATCTCCAGCTG	1015
197	AlaProThrAlaThrCysSerPro-----Pro	205
1016	TGTCACCTGTCTCTCG-----CGTGTCTGTTATAAAAGAAATCTCTACCTGTCTTAG	1072
206	SerAlaA-rgSerAlaTrpLysProCysAlaCysAlaLysAlaValGlySer-----	222
1073	CGGCGCTCGCGATGGGCTGTGG-----CTGTGTTTCCCGTGTGGGGGACCCCAAGG	1129
223	AlaArgSerProAlaAsnAlaTrpProAlaAlaSerAlaTrpCys-----	237
1130	ACAGCTGTCTTACTGTGTGCACACAGCCCAACAGGTCGAGTTCAGATTCGGGATG	1189
238	-----ProThrCysAsnSerAlaA-rgProSerAlaAlaAlaSerThrAlaA-rgAr-g	254
1190	-----AAGACGCACGGCAGA-----ACCCCTACCCAGTGAAGG	1222

Db	255	SerProSerThrAsnGlyArgProAlaAlaCysProThrThrThrProProAlaAsnAla	274
QY	1223	CCA-----TGGAGGTGG-----	1234
Db	275	ProAlaSerAlaAlaAlaAsnTrpProTrpTpyLysAlaProSerProAlaMetProPro	294
QY	1235	TCACACGGGCTCTGAGG-----TCTGGTCAGCAATGGCCGGGCC	1276
Db	295	SerThrSerAlaThrArgLeuAlaAlaCysGlyHisAspGlyAspAla---GlyArgAla	313
QY	1277	TCC-----ATTGTCATCGACTGTGCCT-----CCCTGGAGATCT	1309
Db	314	SerGlnThrProTrpArgAspThrSerProCysValProAsnCysValAsnTrpArgArg	333
QY	1310	CGACGGGCTGGAGC-----CCTCATGGCCC-----CCT	1339
Db	334	ArgIleProTrpSerAlaValAlaIuysThrSerProTrpProA-gTrpProGlyMetPro	353
QY	1340	CCATGGTTACCTCAGTCGTGTCAGCT-----	1366
Db	354	AlaGlyProArgProSerCysThrAlaValAlaAlaTrpAlaProAlaArgGlyGlyTyr	373
QY	1367	-----CTGAGGGCAGGGGAGGAGGAGTCG	1390
Db	374	AlaAlaAlaProArgAsnSerCysSerAlaGlyArgLeuArgArgValArgSer	393
QY	1391	ICT---GGTGCTGGATGACAGGGCAACTCTTGGTGATGTACCACCTCCA-----	1438
Db	394	AlaArgArgAlaIatrp-----ArgProTrpProAlaGlyArgAlaThrProAlaSerAsp	411
QY	1439	-----CCACCTACC-----	1447
Db	412	AlaArgArgAspSerAlaSerArgGlyArgProAlaThrAlaAlaAspHisProAlaAla	431
QY	1448	-----AGCTGTGGCCGCTACTCT-----GGGGGTCCCCAGCCGCCCTCA	1489
Db	432	TrpValSerAlaAlaArgArgThrSerSerAlaProIleAlaGlySerAlaProGlySer	451
QY	1490	GGGACA-----TGTTTCCCG-----TGCGCCCTTGGACA-----	1519
Db	452	GlyThrAlaProArgCysHisProValArgLysAspGlyAlaGlyProAlaSerThrGly	471
QY	1520	CGGAACCCCGGACGAGCCACCGGCCAACCCAAAGTGCTGAGGGGAGCTCCATCG	1579
Db	472	ArgSerArgArgTrpAlaAlaAlaProAlaAlaArgArgAlaArgThrGlyIleArgArg	491
QY	1580	CGGACGTGAGCATCATCT---ACAGTGAGGAGCTGGGACGAGATCTCTGATCACCACAGG	1636
Db	492	ThrAlaAlaAlaAlaCysTyrProProProAlaProGlyArgArgThrProAlaAlaArg	511
QY	1637	AATCACTCACTGACTACTGTCTCATGTCTCTTACTCTTCATCCCAACCCGCGCAGG---	1693
Db	512	ArgArgSerAlaAla-gThrAlaProA-gProAlaIleProAlaHisArgProSerAlaSer	531
QY	1694	-----CTGCCAGGTCGCCCTCAAGCTCCCGAGCTCCCGAGTCCCGACAAAGTTCTTCCAGTG	1744
Db	532	AlaThrGlyTyrProGlyProAlaLeuAlaCysProAlaAlaAlaGlyArgArgPro---	550
QY	1745	TGCCTTTTCCACCGACTCGGAGACTCAGACATGCTACATACGCCCGGTGTCCTCCG	1804
Db	551	-----SerProAlaProAlaProAla-----	557
QY	1805	ACAGTCTGAGCATGACCTGACCCCATGGACGGGGAGACCTTCAGCCAGCACCTGCAGG	1864
Db	558	-----ProAlaProHisAlaArgProArgAlaProArgArgArg	570
QY	1865	CGGTGAGATCC---TGCCGCTCAGAGACCTCATTTGGGTCCCGGCGCGGTGAGATG	1921
Db	571	ProGlyArgSerProAlaThrAlaProAlaAlaPheAlaAlaProAlaGlyProThrPro	590
QY	1922	TTATCGTCATTGGCTGGAGAGGATTCTGAGGCCACGAGGGGGCGAGTCATTGCCGCT	1981

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591 AlaArg-----ProProAlaAlaAlaThrGlyArgProSer 602
1982 TAAAGCCCGAGAGCTGACTCCTGCATGGGTGCTGGTGAATGCTCGTGCAAGG 2041
      |||          |||          |||          |||
603 AlaProProAlaArgAgValArgTp-----ProTrp-----Arg 617
2042 ACACGTGTGTGTCGACCTTTCAAATAAACAACAGAGTGTGTGCCCTGTGGAGG 2101
      ::::||||||| :::::|||
618 SerAlaArgCySerProArgAgProThrProArgSerAla-----ProgLyAlaAla 635
      ::::||||||| :::::|||
2102 GTGGGGGCCGCGAGGTTCACATTTCCTACCAGTCCTTACGAGG 2146
      |||         |::|       |||
636 ThrGlyAlaPro-----ThrThrGlyAlaAlaArgProArggarg 648

ULT 2
18-395-580-2
Sequence 2, Application US/08395580
Ident No. 5676945
GENERAL INFORMATION:
APPLICANT: Usharani R. Reddy, David Pleasure and the Children's
APPLICANT: Hospital of Philadelphia
TITLE OF INVENTION: NO. 5676945E1 Protein Kinase, Nucleic Acid
TITLE OF INVENTION: Sequences Encoding the Same and Methods Related Thereto
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5676945ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
APPLICATION NUMBER: US/08/395,580
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205,018
FILING DATE: 01-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca L. Ralph (formerly Gaumond)
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: CH-0488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
18-395-580-2

Invent Scores:
Seq. Id. No.: 2,14e-14 Length: 859
Matches: 295/50 Mismatches: 168
Percent Similarity: 34.2% Conservative: 89
Local Similarity: 22.4% Indels: 237
Gap Match: 7.28% Gaps: 31
1

19-836-392-8_COPY_22_2205 (1-2184) x US-08-395-580-2 (1-859)
28 GCCATGAAGAARTCTTCGAGTTCGGCAG---GAGGCCAGCATGCTGCAAGCGCTCAC 84
    |||:|||||
150 AlavalysLysValArgAspLeuYsgluThrAspIleYlsHieLysLeuLys 169
    ::::|||||
85 CACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCAACCCGCTGTGCTCGCC----- 138

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494 nValProGlnAsnLeuSer-----ProHisSerGlnArgProAspIleLeuLysAl 511
1015 GTGGTACCTGCTTCTTGGCCGCTGCTGTTATTAAGAATTCCTACCTGGTCTTAGCG- 1074
511 aGluSer-----LeuLeuProLysLeuAspAlaAl 521
1075 GGCTCGCGATGGCTGTGTGCTGTGTTTCCGTGGTGGCGGACCCCAAGGACAGC 1134
521 aLeuSerGlyValGlyLeu----- 527
1135 TGCTCTACTGTGCTCACACAGCCACAGGTCCAAGTTCAGCATCGCGATGAGAC 1194
528 -----ProGlyCysProLysAlaProProSer---ProGlyArgSerArgGlyLysTh 545
1195 GCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGTGGTCAACAGCGGCTCAGGTC 1254
545 rArgHisArg-----LysAlaSerAlaLys 553
1255 TGGTACAGCAATGGCGCGGCTCTTGTTCATCGACTGTGCTCCTCGGAGATCTGCAGG 1314
553 sGlySerCysGlyAspLeuProGlyLeuArgThrAlaValProProHisGluProGlyG 573
1315 CGGCTCGAGCCCT-----ACATGGCCC-----CTCCATG 1344
573 yProGlySerProGlyGlyLeuGlyGlyGlyGlyProSerAlaThrGluAlaCysProProAl 593
1345 GTTACGT-----CA 1353
593 aLeuArgGlyLeuHisAspLeuLeuArgLysMetSerSerSerSerProAspLe 613
1354 GTGGTGTGAGCTCTGAGGCGGAGGAGGAGTGTGCTGGTGGCTG-----ATGAC 1407
613 uLeuSerAlaAlaLeuGlySerArgGlyArgGlyAlaThrGlyAlaGlyAspProG 633
1408 AAGCCCAACTCTTGTGTGATACCACTCCACACTACCACTGTGCTGGTACTTC 1467
633 ySerProProAlaArgLysAspThrProProSerGluGlySerAlaProGlySerTh 653
1468 TGGC-----GGTCCCGAGCCCTCAGGACATGTTTCCC 1503
653 rSerProAspSerProGlyGlyAlaLysGlyProProPro-----Pr 668
1504 GTGGGGCCCTGACACGGAACC-----AACCAGAGTGCCTGAGGGGACTCCATC 1578
668 ovalGlyPro-GlyGlyGlyValGlyLeuGlyThrGlyArgGlyGlyThrSerGlyA 688
1527 -----CCGGCAGCAGCCACACGCCC----- 1548
688 rGlyGlySerArgAlaGlySerGln-HisLeuThrProAlaAlaLeuLeuThrArgAla 707
1549 -----AACCAGAGTGCCTGAGGGGACTCCATC 1578
708 AlaValThrArgSerGlnLysArgGlyLeuSerSerGluGluGluGluValAsp 727
1579 CGGACGTGAGCATCATGTACGTAGGAGAGTGGGACCGACATCTGTATCCACAGGAA 1638
728 SerGluValGluLeuThrSerSerGlnArgTrpProGlnSerLeuAsnMetArgGln--- 746
1639 TCATCTACTGACTCTGCTCATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1698
747 -----SerLeuSerThrPheSerSerGluAsnProSerAspGlyGlu 760
1699 AGGTCCCCCTCAAGCCCTCCAGCAAGTTCCTTCCAGTGTGCTTCTTCCACC 1758
761 GluGlyThrAlaSerGluPro---SerProSerGlyThrProGluValGly---SerThr 778
1759 GACTGCGAGGACTCAGACATCATACACCCCGGTGCTGCTCCACAGGTCTGAGCAT 1818
779 AsnThrAspGluArgProAspGluArgSerAspMetCysSerGlnGlySerGluLe 798
1819 GACTGTGACCCCGGCGGAG 1842
799 ProLeuAspProProProSerGlu 806

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RESULT 3
PCT-US95-02792-2
Sequence 2, Application PC/TUS9502792
GENERAL INFORMATION:
APPLICANT: Usharani R. Reddy, David Pleasure and the Children's
APPLICANT: Hospital of Philadelphia
TITLE OF INVENTION: Novel Protein Kinase, Nucleic Acid
TITLE OF INVENTION: Sequences Encoding the Same and Methods Related Thereto
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02792
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205,018
FILING DATE: 01-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca L. Ralph (formerly Gaumond)
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: CH-0488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-02792-2

Alignment Scores:
Pred. No.: 2,148-14 Length: 859
Score: 295.50 Matches: 168
Percent Similarity: 34.2% Conservative: 89
Best Local Similarity: 22.4% Mismatches: 257
Query Match: 7.28% Indels: 236
DB: 5 Gaps: 31

US-09-836-392-8_COPY_22_2205 (1-2184) x PCT-US95-02792-2 (1-859)
QY 28 GCATGAAGAACTTCCGAGTTCGGCAG---GAGGCCAGCATGCTGCACGCGTGCAG 84
Db 150 AlaValLysValArgAspLeuLysGluThrAspLysHisLeuArgLysLeuLys 169
QY 85 CACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCGCTCTGCTCGCC----- 138
Db 170 HisProAsnIleThrPheLysGlyValCysThrGlnAlaProCysTy-CysIleLeu 189
QY 139 CTGAGACTCGCGCGCTCAGCAGCTCAACCGCTGCTGCTCGGAGAACGCCAGATTCT 198
Db 190 MetGluPheCysAlaGlnGlyGlnLeuTyGluValLeuArgAlaGlyArg----- 206
QY 199 TCCTTTATACCTCGGACACATGCTCACCCCAAAATAGCTTACAGATCGCTCGGCG 258
Db 207 -----ProValThrProSerLeuValAspTrpSerMetGlyIleAlaGlyGly 223
QY 259 CTGCGCTACTCGACAGAAACATCATCTTCTGTGACCTGAGTCGACACATTCTTG 318
Db 224 MetAsnTyrlleuHisLeuHisLysIlelleHisArgAspLeuLysSerProAsnMetLeu 243

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319 GTGTGTCCTTTCAGCTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGATTTCG 378
   ::::::::::::::::::::-VallysileSerAspPheGlyThrSer 258
244 IleThrTyAspAspVal-----
379 AGGCGAG--TCATTCCATGAGGGCGCCCTAGGCTGGAGGGCACTCTCGCTACCAGGCC 435
   ::::::::::::::::::::-MetAla 278
259 LysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThrValAlaTrpMetAla 278
436 CCAGAGATCAGGCCCTCGCATTTGTATATCATGAGAGGTAGATATGTTCTCTATGGAATG 495
   ::::::::::::::::::::-ProGluVal 298
279 ProGluValIleArgAsnGluProValSerGluLysValAspIleTrpSerPheGlyVal 298
496 GTGCTCTACGAGTCTCTCAGGACAGCGCCCT----- 528
299 ValLeuTrpGluLeuLeuThrGlyGluLeuProTyrLysAspValAspSerSerAlaIle 318
529 -----GCATCGGGCCACACCCAGCTCCAGATTCGCAAGAGCTGTCACAGGGCATCCGC 582
319 IleTrpGlyValGlySerAsnSerLeuHisLeu----- 329
583 CGGTTCTGGGCGACCGGAGAGTGCAGTTCGGCGAGCTGCAGGCGCTCATGATGGAG 642
330 ProValProSerSerCysProAsp-----GlyPheLysIleLeuLeuLeuArgGln 345
643 TGTGGGACACTAAGCCAGAGAGCGACG-----CTGGCCCTCTCG 684
346 CysTrpAsnSerLysProArgAsnArgProSerPheArgGlnIleLeuLeuHisLeuAsp 365
685 GTGTGGGACGATGAGGAGCCGACTTTTCCACCTTCATGTATGAACTGTGCTGGG 744
366 IleAlaSerAla-----AspValLeuSerThr 374
745 AAGCAGACAGCCTTCTCTCATCCAGGGCCAG-----GAGTAC 783
375 ProGlnGluThrTyPheLysSerGlnAlaGluTrpArgGluGluValLysLeuHisPhe 394
784 ACCGTGCTGTTTGGGATCGA----- 804
395 GluLysIleLysSerGluGlyThrCysLeuHisArgLeuGluGluLeuValMetArg 414
805 ----AAGAGGATCCAGAAC----- 822
415 ArgArgGluGluLeuArgHisAlaLeuAspIleArgGluHisTyrGluArgLysLeuGlu 434
823 -----TACAGGTGTGTGAACACA-----GAG 843
435 ArgAlaAsnAsnLeuTyMetGluLeuAsnAlaLeuMetLeuGlnLeuGluLysGlu 454
844 AAGGGCTCATGAGGTGCAGAGGATGTGC-----TGCCCTGGGATGAAGGTGAGC 894
455 ArgGluLeuLeuArgArgGluGlnAlaLeuGluArgArgCysProGlyLeuLeuLys-Pr 474
895 TGCCAGCTCCAGTCCAGAGATCCCTGTGGACAGCCCGAGGACCAAAATCTACATC 954
474 ohisProSerArgGlyLeuLeuHisGlyAsnThrMetGluLysLeuLysLysArgAs 494
955 TACACCTCAAGGGCATGTGCCCTTAAACACACCCAGGCTTGGATCTCCAGCT 1014
494 nValProGlnAsnLeuSer-----ProHisSerGlnArgProAspIleLeuLysAl 511
1015 GTCTGTCACCTGCTTCTTGCCGCTGCTGTATTAAAGAAATTCCTACCTGGCTTAGCG 1074
511 aGluSer-----LeuLeuProLysLeuAspAlaAl 521
1075 GGCCTCGCCGATGGCTGTGGCTGTGTTTCCGTGTGGTGGCGGCAACCCAAAGGACAGC 1134
521 aLeuSerGlyValGlyLeu----- 527
1135 TGCTCTCTCTGCTGTCTACACACACGCCAACAGGTCCAAAGTTCACATCGCGGATGAAGAC 1194
528 ----ProGlyCysProLysAlaProProSer---ProGlyArgSerArgGlyLysTh 545
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1195 GCACGGCAGAACCCCTACCAGTGAAGGCCATGAGGTGTCACAGCGGCTCTGAGTTC 1254
   ::::::::::::::::::::-LysAlaSerAla 553
545 rArgHisArg-----
1255 TGGTACAGCAATGGCGCGGCTCTTGTTCATCGACTGTGCTCCCTCGGAGATCTCAGG 1314
   ::::::::::::::::::::-ProHisLeuProGly 573
553 sGlySerCysGlyAspLeuProGlyLeuArgThrAlaValProHisLeuProGly 573
1315 CGGCTGGAGCCCT-----ACATGGCCCC-----CCTCCATG 1344
573 yProGlySerProGlyLeuGlyGlyProSerAlaTrpGluAlaCysProAla 593
1345 GTTACGT-----CA 1353
593 aLeuArgGlyLeuHisAspLeuLeuArgLysMetSerSerSerSerProAspLe 613
1354 CTCGTGTGCAGCTCTGAGGCGCAGAGGGAGGAGTCTGTGTGGCTCGTGG-----ATGAC 1407
613 uLeuSerAlaAlaLeuGlySerArgGlyArgGlyAlaThrGlyGlyAlaGlyAspProG 633
1408 AAGGCCAATCTTGTGTGATGATACCTCCACACCTACCAGCTGTGTGCCCGTACTTC 1467
633 ySerProProProAlaArgGlyAspThrProProSerGluGlySerAlaProGlySer 653
1468 TCGC-----GGGTCCCGCCAGCCCTCAGGACATGTTTCCC 1503
653 rSerProAspSerProGlyGlyAlaLysGlyGluProProPro-----Pr 668
1504 CTGGCGCCCTTGGACACGGAACC----- 1526
668 oValGlyPro-GlyGluGlyValGlyLeuLeuGlyThrGlyArgGlyThrSerGlyA 688
1527 -----CCGCGCAGCCAGCACACGCGCC----- 1548
688 rgGlyGlySerArgAlaGlySerGln-HisLeuThrProAlaAlaLeuLeuTyArgAla 707
1549 -----AACCAGAGTGTGCTGAGGGGACTCCATC 1578
708 AlaValThrArgSerGlnLysArgGlyIleSerSerGluGluGluGlyGluValAsp 727
1579 CGGACGTGAGCATCATGTACAGTGAGGAGCTGGCAGCAGATCTGTATCCACAGGAA 1638
728 SerGluValGluLeuThrSerSerSerGlnArgTrpProGlnSerLeuAsnMetArgGln--- 746
1639 TCACTCACTGACTACTCTCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1698
747 -----SerLeuSerThrPheSerSerGluAsnProSerAspGlyGlu 760
1699 AGTCCCTCCCTCAAGCCTCCCGAGCTCCCGAGCAAGTCTCTCCAGTGTGCTTCTCCACC 1758
761 GluGlyThrAlaSerGluPro---SerProSerGlyThrProGluValGly---SerThr 778
1759 GACTGCGAGGAGCTCAGACATGCTACATACCGCCGGTGTCTGCTCCGACAGGTCTGAGCAT 1818
779 AsnThrAspGluArgProAspGluArgSerAspMetCysSerGlnGlySerGluLe 798
1819 GACTGACCCCGCATGGAGCGGGAG 1842
799 ProLeuAspProProProSerGlu 806

RESULT 4
US-09-345-473E-19
; Sequence 19, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
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1597 ACATGATGCTACGTCGCGATGGAGTGCCTCCCTCAGGCACCTTTGGGTGGCCCTGTGGC 1538  
268 -----ThrProAlaAsnAlaProAlaSerAlaAlaAlaAsnTrpProTrpTyr 285  
1537 TGCGCTCCGGGGTTCGCTGTCACAGGCGCGACGGGAACA-----TGTCCTC 1490  
286 LysAlaProSerProAlaMetProSerThrSerAlaThrArgLeuAlaAlaCys--- 304  
1489 TGAGGGGGTGGGGACCGCGCAGAGTACCGGCACACAGTGTGTAGTGGTGGAGTGGT 1430  
305 -----GlyHisAspGlyAspAlaGlyArgAlaSerGlnThrProTrpArgAsp 320  
1429 ACATCACCAGGAGTGGCTGTGTCATCCAGGCACACAGCAGCCTCTCCCTCTGCCCT 1370  
321 ThrSerProCysValProAsnCysValAsnTrpArgArgArg-----IlePro 336  
1369 CAGAGTGCACAGCTGACGTAACCAATGG----- 1340  
337 TpsrAlaValAlaLysThrSerProTrpProArgTrpProGlyMetProAlaGlyPro 356  
1339 AGGGGCGCATGTAGGCTCCAGCCCGCTGCAGATCTCCAGGAGGCGACGTGATGACAA 1280  
357 ArgProSerCysThrAlaValAlaAlaTrp---AlaProAlaArg----- 370  
1279 GGAGGC-----CGGCCCATTTGCTGTACC----- 1256  
371 GlyGlyTyrAlaAlaAlaProArgAsnSerCysSerAlaGlyArgLeuArgArgVal 390  
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391 ArgArgSerAlaArgAlaTrpArgProTrpProAlaGlyArgAlaThrProAlaSer 410  
1219 -----TCACTGGTAGGGTCTGCGGCTCTCTCATCCGCGA 1181  
411 AspAlaArgArgAspSerAlaSerArgGlyArgProAlaThrAlaAlaAspHisPro--- 429  
1180 TGCTGAACCTTGACCTGTGGCTGTGTGAGCACAGGTAGGACAGCTGTCTTTGGGG 1121  
430 -----AlaAlaTrpValSerAlaAlaArgArgThrSerSerAlaProIleAla 445  
1120 TGCCCGCAGCAGGGAA---ACACAGCCCAAGCCCAT-----CGCGCA 1079  
446 GlySerAlaProGlySerGlyThrAlaProArgCysHisProValArgLysAspGlyAla 465  
1078 GCGCCCTAAGACCGAGTGGTAATCTTTTAATAACAGGACCGCCCAAGAGCAGTGA 1019  
466 GlyProAlaSerThrGlyArgSerArgArgTrpAlaAlaAlaProAlaArgArgAla 485  
1018 CGACAGCTGGAGTATCCAGGCGCTTGGGGTGTGTTTAAGGGGCACATGCCCTTGAGGG 959  
486 Arg----- 486  
958 TGTAGATGTAGATTTTCTGCTCGGTGCTGTCACAGGATCTCTGGACCTGGAGCT 899  
487 -----ThrGlyIleArgArgThrAlaAla 494  
898 GGCAGCTACCTTATCCAGGCGCAGCAGCATCTCTGCACCTCCATGCCCTTCTCTG 839  
495 AlaAla----- 496  
838 TGTTCCACACCGTGTAGTCTCTGGACTCTCTTTCCATCCAAAACACACCGGTGACT 779  
497 CysTyrProPro-----ProAlaProGlyArgArgThr 507  
778 CTGGCGCTGGGATGAGAAGAGGCTGTCTGCTCCACAGCAGCATGTTTCATCATGAAG 719  
508 ProAlaAlaArgArgSerAlaArgThrAlaProArgProAlaIleProAlaHisArg 527  
718 TGCGAAAGTCGGGTCTTCATCTGGCTCACCAGCAGGCGCAGGCGTCTCTCTG 659  
528 -----ProSerAlaSerAlaThrGlyTrpPro-----GlyProAlaLeuAla----- 541

QY 658 GCTTAGTGTCCAGC-----ACTCATCATGAGCGCTGCGAGTGGCC 617  
Db 542 -----CysProAlaAlaAlaGlyArgArgProSerProAlaProAlaProAla 559  
QY 616 GGAACCTGCACTTCTCCGGCT---GCCCCAGAACCGGGCGGATGCCCTTGCACAGCTTCT 560  
Db 560 ProHisAlaArgProAlaAlaProAlaArgArgProGlyArgSerProAlaThrAlaPro 579  
QY 559 TGGCAATCTGGAGTGTGTGGTGGCCAGTGCAGGGC-----GCTTCCTGACAGCA 509  
Db 580 AlaAlaPheAlaAlaProAlaGlyProThrProAlaArgProProAlaAlaAlaThrGly 599  
QY 508 ACTCGTAGAGCA-----CCATTCCATAGAGACATATCTACCTTCTCATATATA 458  
Db 600 ArgProSerAlaProProAlaArgProAlaArgArgValArgTrpProTrpArg----- 617  
QY 457 CAATCGAGGCTGATCTCTGGGCGCTGGTAGCCAGGAGTGCCTCCACGCTAGGCGC 398  
Db 618 -----SerAlaArgCysSerProAlaArgProThr 627  
QY 397 CCTCATGGAATGACTGCTCGAATCCGCTAGTGCAGATAGCTTGTGATGTTGATGCTCCT 338  
Db 628 ProArgSerAlaProGlyAlaAlaThrGlyAla----- 638  
QY 337 TCAGCTCAAGGCGCACACACAGAGATGTGTCGACCTTCAGGTACAGAGATGATGTTT 278  
Db 639 -----ProThrThrGlyAlaAlaArgProAlaArg 648  
QY 277 TCTTGTGAGTAGGCGCAGGCGCGAGCTCTGGTAGG 239  
Db 649 ArgAlaAlaAlaProGlyLysArgArgSerAlaArg 661

RESULT 6  
US-08-205-018-2  
Sequence 2, Application US/08205018  
Patent No. 5554523  
GENERAL INFORMATION:  
APPLICANT: Reddy, Usharani R.  
APPLICANT: Pleasure, David  
TITLE OF INVENTION: No. 5554523el Protein Kinase, Nucleic Acid  
TITLE OF INVENTION: Sequences Encoding the same and Methods Related  
TITLE OF INVENTION: Thereto  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
ADDRESSEE: No. 5554523ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/205,018  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaumont, Rebecca R.  
REGISTRATION NUMBER: 35,152  
REFERENCE/POCKET NUMBER: CH-0488  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 668 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

8-205-018-2

Instrument Scores:

i. No.:	2.9e-12	Length:	668
e:	267.00	Matches:	139
ent Similarity:	34.86%	Conservative:	67
: Local Similarity:	23.52%	Mismatches:	206
y Match:	6.58%	Indels:	179
		Gaps:	26

)9-836-392-8 COPY 22 2205 (1-2184) x US-08-205-018-2 (1-668)

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85 CACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCGCTCTGCTTCCGCC--- 138  
170 HisProAsnIleIleThrPheLysGlyValCysThrGlnAlaProCysTyrCysIleLeu 189  
139 CTGAGCTCGCCGCTCAGCAGCCTCAACACCGTCTGTCGAGAACGCCAGAGATTCT 198  
190 MetGluPheCysAlaGlnGlyGlnLeuTyrGluValLeuArgAlaGlyArg----- 206  
199 TCCTTTATACCCCTGGGACACATGCTCACCCCAAAAAATAGCTACACATCGCTCGGCG 258  
207 -----ProValThrProSerLeuLeuValAspTrpSerMetGlyIleAlaGly 223  
259 CTGGCCTACCTGCACAAAGAAAAACATCATCTTCTGTGACCTGGAAGTCGACAACTTCG 318  
224 MetAsnTyrLeuHisLeuHisLysIleIleHisArgAspLeuLysSerProAsnMetLeu 243  
319 GTGTGTCCTTGCATCAGGAGACATCATACATCAAGCTATCTGACTAGGGATTTCG 378  
244 IleThrTyrAspAspVal-----ValLysIleSerAspPheGlyThrSer 258  
379 AGGCAG-----TCATTCCATCAGGCGCCCTAGCGTGGAGGGCAGCTCCTGGCTACCAGGCC 435  
259 LysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThrValAlaTrpMetAla 278  
436 CCAGAGATCAGGCCTCGCATTTGATATGATGAGAGGTAGATATGTTCTCTATGGAATG 495  
279 ProGluValIleArgAsnGluProValSerGluLysValAspIleTrpSerPheGlyVal 298  
496 GTGCTCTACGAGTTGTGTGCAGACAGCCCT----- 528  
299 ValLeuTrpGluLeuLeuThrGlyGluIleProTyrLysAspValAspSerSerAlaIle 318  
529 -----GCATCGGCCACCACCAAGCTCCAGTTCGACAGAGCTGCCAAGGGCATCCGC 582  
319 IleTrpGlyValGlySerAsnSerLeuHisLeu----- 329  
583 CCGGTTCTGGGGCAGCCGGAGAGTGTCAGTTCGGCGAGCTCGAGCGCTCATGATGAG 642  
330 ProValProSerSerCysProAsp-----GlyPheLysIleLeuLeuArgGln 345  
643 TGTGTGGACACTAAGCCAGAGAGCGACCG-----CTGCGCCCTGTGC 684  
346 CysTrpAsnSerLysProArgAsnArgProSerPheArgGlnIleLeuLeuHisLeuAsp 365  
685 GTGTGTGACCATGAGGACCGCACTTTTGCCACCTTCATGTATCAACTGTGCTGTGG 744  
366 IleAlaSerAla-----AspValLeuSerThr 374  
745 AAGCAGACAGCGCTTCTTCATCCAGGGCCAG-----GAGTAC 783  
375 ProGlnGluThrTyrPheLysSerGlnAlaGluTrpArgGluGluValLysLeuHisPhe 394  
784 ACCGTGTGTTTTGGGATGGA----- 804  
395 GluLysIleLysSerGluGlyThrCysLeuHisLeuGluGluValMetArg 414  
805 ---AAGACGAGTCCAGGAAC----- 822

Db	415	ArgArgGluGluLeuArgHisAlaLeuAspIleArgGluHisTyrGluArgLysLeuGlu	434
Qy	823	-----TACAGGTGGTGAACA-----CAG	843
Db	435	ArgAlaAsnAsnLeuTyrMetGluLeuAsnAlaLeuMetLeuGlnLeuGluLeuLysGlu	454
Qy	844	AAGGGCTCATGGAGGTGCAGGATGTGC-----TGCCCTGGGATGAAGTGCAGC	894
Db	455	ArgGluLeuLeuArgArgGluGlnAlaLeuGluAaGArgCysProGlyLeuLeuLys-Pr	474
Qy	895	TGCCAGTCTCCAGTCCAGATCCCTGTGGACAGCCACCGAGGACCAAAATCTACATC	954
Db	474	OhieProSerArgglyLeuLeuHisglyAsnThrMetGluLysLeuIleLysLysArgAs	494
Qy	955	TACACCTCAAGGCGATGTGCCCTTAAACACACCCACAGCGCTTGGATACTCCAGCT	1014
Db	494	nValProGlnAsnLeuSer-----ProHisSerGlnArgProAspIleLeuLysAl	511
Qy	1015	GFCTGTCACTCTCTTGGCCGTGCCTGTATTATAAAAGAAATCTCACTCGTCTTAGCG	1074
Db	511	aglUser-----LeuLeuProLysLeuAspAlaAl	521
Qy	1075	GGCTTCGCGGATGGCTTGTGGCTGTCTCCGCTGTCGGGGCACCCCAAGACAGC	1134
Db	521	aleuSerGlyValGlyLeu-----	527
Qy	1135	TGCTCTCACTGTCTCACACAGCCACAGGTCCAAGTTCAGCATCCGGATGAAGAC	1194
Db	528	----ProGlyCysProLysAlaProProSer--ProGlyArgSerArgArgLysTh	545
Qy	1195	GCACGGCAGACCCCTACCAGTCAAGGCCATCGAGGTGGTCAACAGCGGCTCTGAGTC	1254
Db	545	xArgHisArg-----LysAlaSerAlaLys	553
Qy	1255	TGGTACAGCAATGGCGCGGCTCTTGTCATCGACTGTGCCTCCCTCGAGATCTGCAGG	1314
Db	553	sglySerCysglyAspLeuProGlyLeuArgThrAlaValProHisGluProGlyGly	573
Qy	1315	CGCTGGAGCCCT-----ACATGCC-----CCTCCATG	1344
Db	573	yProGlySerProGlyGlyLeuGlyGlyProSerAlaIrrpGluAlaCysProProAl	593
Qy	1345	GTTAGCT-----CA	1353
Db	593	aleuArgGlyLeuHisAspLeuLeuArgLysMetSerSerSerSerProAspLe	613
Qy	1354	GTCGTGTGAGCTCTGAGCGCAGAGGAGAGGTCTGTGTGTCCTGG-----ATAC	1407
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Qy	1408	AAGGCCAACTCTGTGTATCTACCTCCACCAACCTACAGCTGTGTGCCCGGT---AC	1464
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Qy	1465	TTCTGCGGGGTCCCGAGCC---CCTCAGGG	1492
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## RESULT 7

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RESOLUT - 7
US-09-252-991A-26129
, Sequence 26129, Application US/09252991A
, Patent No. 6551795
, GENERAL INFORMATION:
, APPLICANT: Marc J. Rubenfield et al.
, TITLE OF INVENTION: NUCLEIC ACID AND AMINO
, TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOS
, FILE REFERENCE: 107196.136
, CURRENT APPLICATION NUMBER: US/09/252,991A
, CURRENT FILING DATE: 1999-02-18
, PRIOR APPLICATION NUMBER: US 60/074,788
, PRIOR FILING DATE: 1998-02-18
, PRIOR APPLICATION NUMBER: US 60/094,190

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535 CCAGTGCAGGGCGTCTCTGACAGCAACTGTGTAGACCACTTCAT-----AGGAGA 482  
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605 ProAlaGlyArgValGlyGlyArgGluAlaGlyArgGlnProAlaTyrProGlyArgGly 624  
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481 ACATATCTACCTTCTCATCATATACAAATGCGAGCCCTGATCTCTGGGCGCTGTGTACCAAG 422  
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625 -----ProAlaHisLeuGlnArgArgAlaGluSerArgGlyProGlyProGlu 641  
|||  
421 GAGTGCCTCCACGCCCTAGGCGC-----CCTCATGGAATGATGCTCTG 377  
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642 ProAlaGlnGlyGluValGlyGlnPheProAlaGluLeuLeuHisGlyLeuProAlaA-Arg 661  
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376 AAATCCCGTAGTCAGATAGCTTGATGTGTGATGCTCTTTCAGCTCAAGGACCAACACCA 317  
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661 GHisProAspArgProAlaGlyAspLeu-----ProAspGln 673  
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316 GAATGTTGTCGACTTTCAGGTCACAGAAGATGATGTTTTTCTTGTGCGAGGTAGCCAG-- 259  
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673 n-----LeuLeuProAlaGlyGlnPro 680  
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258 -----GCCCGAGCGCATCTGGTAGGCTATTTTTTG----- 229  
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680 GglyThrArgProAspArgThrGlyProArgLeuProHisArgHisProAlaAlaGlyArg 700  
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228 -----GGTGAGCATGTCTCCAGCGGTATATAAGAAAGA-----AT 194  
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700 GArgProAlaGluProAlaAlaGluHisProArgProGlyHisProGlyArgGlyValArg 720  
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193 CTCTGGCGTCTTCGACAGACGCGGTGTGAGGCTGTGAGCGGCGAGCTCCAGGG---- 137  
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136 -----CGAAGCAGACGCGGTGGATGCTGATGCCGATGAGCGCCACGATCCAGG--GGT 86  
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740 ProArgArgAlaArgAlaProGlyCys-----ProAlaAlaArgAlaGly 754  
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85 GTCGACGCGCTGCAGCATGTGCGCTCTCTCCGGAAGCTCGAGAACTTCTTCATGGCAT 26  
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755 CysArgAlaArgValAlaAlaThrTyrProAlaGlyArgValArgProAlaAlaArgSer 774  
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25 CGGTGGCGCCGCA 14  
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775 GlnArgProAla 778  
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III.

UL 8  
09-428-711A-16

09-428-711A-16  
equence 16. Application US/09428711A

sequence 16, APPLICATION US/09428/11A  
 atent No. 6358720

GENERAL INFORMATION:

GENERAL INFORMATION:  
APPLICANT: Muramatsu, Masaaki

APPLICANT: MUZUMATSU, MASAHI  
APPLICANT: Shirayawa, Takuji

APPLICANT: SHIRAWAWA, TAKUJI  
APPLICANT: TOKUMITSU, HIROSHI

APPLICANT: TOKUMITSU, HIYOSHI  
APPLICANT: No. 6358720uchi. Teruhisa

APPLICANT: NO: 8358/2000L, REFUNDING  
TITLE OF INVENTION: SERINE/THREONINE

TITLE OF INVENTION: SERINE/THREONINE  
FILE REFERENCE: 06501-045001

FILE REFERENCE: 06301-043001  
CURRENT APPLICATION NUMBER: US/09/42

CURRENT FILING DATE: 1999-10-28  
CURRENT APPLICATION NUMBER: US/09/42

CURRENT FILING DATE: 1999-10-28  
PRIOR APPLICATION NUMBER: PCT/JP98/

PRIOR APPLICATION NUMBER: FCI/JP98/  
PRIOR FILING DATE: 1998-03-23

PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: JP 9/1247

PRIOR APPLICATION NUMBER: JP 9/12477  
PRIOR FILING DATE: 1997-04-28

PRIOR FILING DATE: 1997-04-28  
NUMBER OF SEQ. ID NOS. 21

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 1.6  
 EC ID NO 16

EQ ID NO 16  
ENCLOSURE

LENGTH: 1050  
TYPE: PDF

TYPE: PRT  
ORGANISM: HOMO SAPIENS

ORGANISM: Homo sapiens

09-428-711A-16

gment Scores:

9.9e-12

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re: 261.00

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Percent Similarity: 35.57%

Best Local Similarity:	23.96%	Mismatches:	311
Query Match:	6.43%	Indels:	217
DB:	4	Gaps:	38

US-09-836-392-8\_COPY\_22\_2205 (11-2184) x US-09-428-711A-16 (11-1050)

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QY	115	AGC-----ATCCACCGCTCTGCTTCGCCCTCGAGCTCGCG	150
Db	82	GlnGluMetAlaAsnSerValTyrLeuValMetGluTyrCysAsnGlyGlyAspLeuAla	101
QY	151	CGGCTCAGCAGCCTCAACACGGTCTGTCGAGAACGCCAGACATCTTCTCTTATACCC	210
Db	102	AspTyrLeuHisAlaMetArgThrLeuSerGluAspThr-----	114
QY	211	CTGGCAGACATGCTCACCCAAAATAAGCTACAGATCGCTCGGGCTCGCCCTACCTG	270
Db	115	-----IleArgLeuPheLeuGlnGlnIleAlaGlyAlaMetArgLeuLeu	129
QY	271	CACAGAAAAATCATCTTCTGTGACCTGAATCGGACAACATTCGTGTGTGTCCTT	330
Db	130	HisSerLysGlyIleIleHisArgAspLeuLysProGlnAsnIleLeuLeuSerAsnPro	149
QY	331	GAGCTCAAG-----GAGCACATCAACATCAAGCTATCTGACTACGGGATTTTCG	378
Db	150	AlaGlyArgArgAlaAsnProAsnSerIleArgValLysIleAlaAspPheGlyPheAla	169
QY	379	AGG-----CAGTCATTCCATGAGGCGCCCTAGGCGTGGAGGGCACTCTGGCTACCA	432
Db	170	ArgTyrLeuGlnSer---AsnMetMetAlaAlaThrLeuCysGlySerProMetfyrMet	188
QY	433	GCCACAGAGATCAGCCTCGCATGTATATATGACAGAGTAGATGATTTCTCCATATGA	492
Db	189	AlaProGluValIleMetSerGlnHisTyrAspGlyLysAlaAspLeuTrpSerIleGly	208
QY	493	ATGTGCTCTACGAGTTGCTCTCAGGACGAGCGCCCT-----GCATGGGGCCACCACC	546
Db	209	ThrIleValTyrGlnCyeLeuThrGlyLysAlaProPheGlnAlaSerSerProGlnAsp	228
QY	547	CTCCAGATTGCCAAGAAGCTCTCCAGGCGATCGCGCGTTCTGGCGCAGCGCGAGAA	606
Db	229	LeuArgPhePheTyrGluLysAsnLysThrLeuValProThrIleProArgGluThrSer	248
QY	607	GTCCAGTTCGCGCACTCCAGCGCTCATCATGATGAG-----	642
Db	249	AlaProLeuArgGlnLeuLeuLeuAlaLeuLeuGlnLArgAsnHisLysAspArgMetAsp	268
QY	643	-----TGCTGGGACACTAAGCCAGAGAACGCGCTGTGCC	678
Db	269	PheAspGluPhePheHisProPheLeuAspAlaSerProSerValArg-----	285
QY	679	CTGTCCGTGGTCAGCCACATCAAGGACCCGACTTTGCCA---CCTTCATGATGAAC	735
Db	286	-----LysSerProPro-ValProValProSerTyrProSerSe	298
QY	736	TGCTGTGGGAAGACACAGCCTTCTTCATCCAGGGCCAGAGATACACCGTGTGTTT	795
Db	298	rdgSerGlySerSerSerSerSerSerSerThrSerHisLeuAlaSerProSerLeu	318
QY	796	TGGG-----ATGGAAGAAG-----AGAGTCCAGGACTACACGGTGGT---G	834
Db	318	uGlyGluMetGlnGlnLeuGlnLysThrLeuAlaSerProAlaAspThr-AlaGlyPheL	338
QY	835	AACACAGAGAAGGGCTCATCGAGTGCAGAGAT-----	869
Db	338	euiHisSerSerArgAspSerGlyGlySerLysAspSerSerCysAspThrAspAspPheV	358
QY	870	--GTGCTGCCCTGGGAT---GAAGGTGAGTGT-----CCAGTCCAGGTCCAGAGATCC	918
Db	358	aiMetValProAlaGlnPheProGlyAspLeuValAlaGluAlaProSerAlaLysProp	378

[illegible]

1829 -----CCATGGACGGGAGACCTTCAGCCAGCACCTTCAGCCCGTGAAGA----- 1873

665 erGluValGlyProPheHisGlyGlnProLeuGlyProGlyLeuArgProGlyGluAspP 685

1874 --TCCTCGCGCTCAGAGACCTCAATTTGGGTCCCCAGCGCGGTGGAGATGTTATCGTCAT 1931

685 rolysglyProPheGlyArgSerPheSerThrSerArgLeuThrAspLeuLeuLysA 705

1932 TGGCTGG-----AGAGGATTTCTGAAGCCAGCGGGGCCGAGTCATTGCGCTCTTAAAGC 1988

705 laAlaPheGlyThrGlnAlaProAspProGlySerThrGluSerLeuGlnGluLysProM 725

1989 CCAGAGCTCACTCCGCATCGGGTGTGTTGGGATGCTG---CCGTGGTGGCAAGGACAC 2045

725 etGluLeuAlaProSerAlaGlyPheGlyGlySerLeuHisProGlyAlaArgAlaGlyG 745

2046 TGTGTGTGCACCTTTGAAATGAACACAGAGTGTGCCTGGCGCTGTGGAGGGCTG 2105

745 lyThrSerSerProSerProValPheThrValGlySerProProSerGlySerThrP 765

2106 GGGCGCCAGGAGTTCGACA-----TTTTCTACCAGTCTCTAGGAGC 2149

765 roProGlnGlyProArgThrArgMetPheSerAlaGlyProThrGlySer 781

RESULT 9

US-09-252-991A-21827

; Sequence 21827, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 21827

; LENGTH: 1093

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21827

Alignment Scores:

Pred. No.: 1,2e-11 Length: 1093

Score: 260.00 Matches: 233

Percent Similarity: 31.60% Conservative: 77

Best Local Similarity: 23.75% Mismatches: 352

Query Match: 6.41% Indels: 320

DB: 4 Gaps: 49

US-09-836-392-8\_COPY\_22\_2205 (1-2184) x US-09-252-991A-21827 (1-1093)

Qy 35 AGAATTCTCCGAGTTCGGCAGGAGCCAGCATGTCGACGCGTGCAGC----- 85

Db 44 ArgArgCysProGlyArgTyProArgLeuAlaAlaSerIleArgCysAlaProLeuLeu 63

Qy 86 -----ACCCCTGCATCGGGCGCTCATGGCATCAGCATCCACCGCGTCTGCTCGCCC 139

Db 64 ThrGlnAlaProTrpProThrLeuSerSerAlaProProArgValMetAlaSerPro 83

Qy 140 TGGAGTCTCGCGCGCTCAGCGCTCA-----ACACCGTCG 175

Db 84 SerLeuAlaArgLysGlyAlaAlaGlyAlaValValGlnAlaProAlaTrpSerProSer 103

Qy 176 TGTCGAGACGCGCAGATT-----CTTCCTTTATACCGCTGGGACACATGCTCACCC 229

Db 104 GlyProGlyHisProGluSerArgProAlaProAlaLeuProSerAlaSerArg 123

Qy 230 AAAAAATAGCTTACCAGATCGCTCGG---GCTCGCCCTACCTGCACAGAAAAACATCA 286

Alignment Scores:		
Pred. No.:	1.2e-11	Length:
Score:	260.00	Matches:
Percent Similarity:	31.60%	Conservative:
Best Local Similarity:	23.75%	Mismatches:
Query Match:	6.41%	Indels:
DB:	4	Gaps:
		49
		320
		352
		770
		233
		1093

US-09-836-392-8\_COPY\_22\_2205 (1-2184) x US-09-252-991A-21827 (1-1093)

Qy	35	AGAACTTCTCCGAGTTC	CGGAGGAGCCAGCATGCTGCAGCGCTGCAGC-----	85
Db	44	ArgAgCysProGlyArgTy:ProArgLeuAlaAlaSerIleArgCysAlaProLeuLeu	63	
Qy	86	-----ACCCCTGCATCTGGCGTTCATCGGCATCAGCATCCACCGCTCTGCTGTGGCC	139	
Db	64	ThrGlnAlaProTrpProTrpLeuSerSerAlaProArgValMetAlaSerSerPro	83	
Qy	140	TGGAGCTCGCGCGCTCAGCAGCTCA-----ACACCGTGC	175	
Db	84	SerLeuAlaArgLyGlyAlaAlaGlyAlaValGlnAlaProAlaTyrSerProSer	103	
Qy	176	TGTCGAGAGACCCAGAGATT-----CTTCCTTTATACCCCTGGGACACATGCTCACCC	229	
Db	104	GlyProGlyHisProGlySerArgProAlaProAlaLeuProSerAlaAlaSerArg	123	
Oy	230	AAAAAATAGCCTACACAGATCGCCTCGG---GCCTGGCCTACCTGCACAAGAAAAAATCA	286	

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124 ArgSerPheProAlaLeuMetMetArgProCysTrpProLeuSerMetArgLeuAlaSer 143
    :||| :||| :||| :||| :||| :|||
287 TCTTCTGTG-----ACCTGAAGT 304
    :||| :||| :||| :||| :||| :|||
144 SerSerLysProCysTrpLeuGluLeuSerProProTrpArgLeuSerArgThrPheSer 163
    :||| :||| :||| :||| :||| :|||
305 CGGACAACTTCTGGTGTCTCCCTTGACG-----TCAAGGAGC 343
    :||| :||| :||| :||| :||| :|||
164 ArgSerMetLeu---SerGlyProArgAlaLeuLeuArgProProTrpLeuSerArgSer 182
    :||| :||| :||| :||| :||| :|||
344 ACATCAACATCAAGCTATCTGATCAGGGATTTCGAGCAGTTCATTCATGAGGCGCC 403
    :||| :||| :||| :||| :||| :|||
183 ProProArgArgSerArgLeuThrPro-----ArgSerPro 194
    :||| :||| :||| :||| :||| :|||
404 TAGCGGTGGAGGCGCACTCTGGCTACCGGCCCCAGAGATCAGGCTCGCATTTGATATG 463
    :||| :||| :||| :||| :||| :|||
195 -----ThrSerArgProTrpArgCysThrArgArgSerThrVal 207
    :||| :||| :||| :||| :||| :|||
464 ATGAGAAGGTAGATATGTTCTCTATGGAATGGTCTCTACAGTTGCTGTCAGACAGC 523
    :||| :||| :||| :||| :||| :|||
208 ArgArgArg-----SerProArgAlaGluLeuSerProProSerAlaGluSerThr 224
    :||| :||| :||| :||| :||| :|||
524 GCCTGCACTGGCCACACCGCTCCAGATTGCCAAGAGCTGCCAAGGCGATCCGCC 583
    :||| :||| :||| :||| :||| :|||
225 ArgProAlaValSerSerSerSerProSerLeuValSerArgProProArgLeuSer--- 243
    :||| :||| :||| :||| :||| :|||
584 CGGTTCTGGGGCAGCCGAGGAAGTGCAGTCCGGCGACTGC-----AGCGGC 631
    :||| :||| :||| :||| :||| :|||
244 ArgLeuAlaAlaLeuArg-----SerAspCysLeuProLeuArgAlaPro 259
    :||| :||| :||| :||| :||| :|||
632 TCATGATGAGTGCTGGGACACTAAGCCAGACGACGACCGGTGCTGCTGCTGCTGTA 691
    :||| :||| :||| :||| :||| :|||
260 ProArgLeuSerArgSerAlaLeuLeuThrSerSerThrProTrpLeuLeuAsnTrp--- 278
    :||| :||| :||| :||| :||| :|||
692 GCCAGATGAAGGACCGCACTTTGCCACCTTCATGTAAGTGTGCT---GTGGGAAGC 748
    :||| :||| :||| :||| :||| :|||
279 -----ProProSerAlaLeuSerSerAlaProValAlaThr 290
    :||| :||| :||| :||| :||| :|||
749 AGACAGCTTCTTCTCATCCAGGGCCAGAGTACACCGTGG-----TGTTTT 796
    :||| :||| :||| :||| :||| :|||
291 LeuArgProAlaLeu---ProGluSerArgProLeuProLeuLeuSerArgGluAlaLeu 309
    :||| :||| :||| :||| :||| :|||
797 GCGATGMAAGAGGAGTCCAGGAAGT-----ACACGGTGTGTAACACAGAGGCGCC 850
    :||| :||| :||| :||| :||| :|||
310 AlaSerValArgAlaProGluThrValProSerAlaTrpLeuSerSerAlaProSer 329
    :||| :||| :||| :||| :||| :|||
851 TCATGAGGTGCAGAGGATGT-----GTCGCCCTGGGATGAAG 889
    :||| :||| :||| :||| :||| :|||
330 ThrArgArgSerMetProAlaArgLeuAlaArgValProLeuAlaLeuLeuSerArgArg 349
    :||| :||| :||| :||| :||| :|||
890 TGAGCTGCCAGTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGG-----ACCAGA 943
    :||| :||| :||| :||| :||| :|||
350 AlaAlaAlaMetSerArgProAlaAlaProGluLeuThrProAlaArgLeuLeuSerArg 369
    :||| :||| :||| :||| :||| :|||
944 AAATCTACATCTACACCTCAGGGCATGTGCCCTTAACACACCCCAACAGG----- 997
    :||| :||| :||| :||| :||| :|||
370 AlaTrpAlaMetArgValArgLeuAlaAlaProIleArgArgProProArgLeuSer 389
    :||| :||| :||| :||| :||| :|||
998 -----CCTTGGATCTCCAGCTGCTGCTGCTGCTGCT----- 1027
    :||| :||| :||| :||| :||| :|||
390 ArgLeuAlaAlaAlaArgValLysAlaArgSerLeuGluLeuSerProProAlaProLeu 409
    :||| :||| :||| :||| :||| :|||
1028 -----TCTTGG-----CCGTGCGCTG 1042
    :||| :||| :||| :||| :||| :|||
410 SerThrAlaProSerTrpArgSerSerAlaProGlyValAlaIleArgProProSer 429
    :||| :||| :||| :||| :||| :|||
1043 TTATTAAAGATTTCTACCTGGTCTTAGCGGCTCCCGCATGGGCTGTGGCTGTGT 1102
    :||| :||| :||| :||| :||| :|||
430 ArgLeuThrSerValProProLeuArgSerArgValThrProValSerLeuThrArgThr 449
    :||| :||| :||| :||| :||| :|||
1103 TTCCCG-----TGGTGGGGGACCCCAAGAGCAGCTGCTCCTACCTGCTGCACACA 1156
    :||| :||| :||| :||| :||| :|||

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450 ProProProArgTrpSerArgProPheArgLeuAlaSerSerArgProLeuAlaLeuThr 469
    :||| :||| :||| :||| :||| :|||
1157 CAGCCAAACAGGTCCAGTTCAGCATCGCGATGAAGACGCAC----- 1198
    :||| :||| :||| :||| :||| :|||
470 ArgProCysTrpProLeuSer---SerArgAlaAlaThrArgValMetProAlaLeuLeu 488
    :||| :||| :||| :||| :||| :|||
1199 -----GGCAGAACCCCTACCAGTGAAGGCCATCGAGGTGG 1234
    :||| :||| :||| :||| :||| :|||
489 ProMetProProLeuArgLeuLeuSerSerThrProVal-----ArgIle 503
    :||| :||| :||| :||| :||| :|||
1235 TCAACAGCGGCTCTGAGGTCTGGTACA----- 1261
    :||| :||| :||| :||| :||| :|||
504 SerThrAlaProLeuAlaLeuLeuThrProGluArgLeuLeuSerArgLeuAlaProCys 523
    :||| :||| :||| :||| :||| :|||
1262 GCAATGGCCCGGGCTCTTGTCTCATCGACTGTGCTCCCTGGAGATTCGAGCGCGCTGG 1321
    :||| :||| :||| :||| :||| :|||
524 SerValThrProAlaSerLeuSer---LeuProProTrpLeuSerSerAlaAlaTrp 542
    :||| :||| :||| :||| :||| :|||
1322 -----AGCCCTACATGG-----CCCCCTCATGGTTACCTCAGTCG 1357
    :||| :||| :||| :||| :||| :|||
543 LeuValSerAlaSerAlaProAlaLeuGluLysValProProArgLeuSerArgArgAla 562
    :||| :||| :||| :||| :||| :|||
1358 TGTGCAAGCTCTGAGGGCAGAGGGGAGGAGTCTGCTGCTGCTGCTGATGACAAGGCCAACT 1417
    :||| :||| :||| :||| :||| :|||
563 AlaArgAlaValArgLeuProSerLeuThrSerAlaProProTrpLeuSerSerThrPro 582
    :||| :||| :||| :||| :||| :|||
1418 CCT-----TGTGATGTACCACTCA----- 1438
    :||| :||| :||| :||| :||| :|||
583 ProArgLeuThrLeuArgLeuPheTrpLeuSerSerArgProProSerProLeuAsnSer 602
    :||| :||| :||| :||| :||| :|||
1439 ---CCACCTACAGCTGTGCGCGGTACTTCTGCGGGTCCCCAGGCCCCC-----TCA 1489
    :||| :||| :||| :||| :||| :|||
603 SerProProSerArgLeuArgProSerArgProAlaSerThrProLeuAlaTrpPheSer 622
    :||| :||| :||| :||| :||| :|||
1490 GGGACATTTTC-----CCGTGGCGCCTTGGACACGGAACCCCGG----- 1531
    :||| :||| :||| :||| :||| :|||
623 ArgAspCysThrValArgArgProLeuSerProMetThrLeuProProArgLeuSer 642
    :||| :||| :||| :||| :||| :|||
1532 -----CAGCCAGCACACGCGCCAAACCCAAAGGTGCTGAGGGGACTCCATCGCGACG 1585
    :||| :||| :||| :||| :||| :|||
643 SerCysSerArgAlaPheThrAlaThrPheGluValLeuGluLeuSerProAlaArgLeu 662
    :||| :||| :||| :||| :||| :|||
1586 TGAGCATCATCTACAGTGAGGAGCTGGGACGACGAGATCTCTGATCCACAGGAATCACTCA 1645
    :||| :||| :||| :||| :||| :|||
663 -----SerThrCysArg-AlaSerIleAlaMetProPheAlaAlaIleSerGI 679
    :||| :||| :||| :||| :||| :|||
1646 CTGACTACTGCTCCATGTC-----CTCCTACTCTCATCCCCAC 1684
    :||| :||| :||| :||| :||| :|||
679 nAspTrpLeuLeuSerIleValSerAlaAlaThrPheArgValPheSerLeuThrSerSe 699
    :||| :||| :||| :||| :||| :|||
1685 CCGGCCA-----GGCTGCCAGTCCCCCTC-----AA 1711
    :||| :||| :||| :||| :||| :|||
699 rProProCysTrpAlaArgLeuProSerValAlaCysArgSerProLeuAlaAlaIleAr 719
    :||| :||| :||| :||| :||| :|||
1712 GCTCCCGCAGCTCCCGCAAGTTCTT----- 1738
    :||| :||| :||| :||| :||| :|||
719 gProProAlaLeuProThrAlaPheAlaAlaArgSerArgArgProSerLeuAsnSerLe 739
    :||| :||| :||| :||| :||| :|||
1739 ----CCAGTGTGCTTTCTCCACCGACTCGAGGACTCAGACATGTACATACGCCCGGT 1794
    :||| :||| :||| :||| :||| :|||
739 uProProTrpSerLeuArgLeuAlaThrSerThrArgThrProAlaLeuProLeuAl 759
    :||| :||| :||| :||| :||| :|||
1795 GTGCTCCGAGAGTCTGAGCATGACCTGAGCCC----- 1828
    :||| :||| :||| :||| :||| :|||
759 aLeuProProSerArgLeuSerLysAlaProProValAlaLeuLysProAlaSerAlaTh 779
    :||| :||| :||| :||| :||| :|||
1829 -----CCATGGAGC----- 1837
    :||| :||| :||| :||| :||| :|||
779 rSerThrProProArgLeuSerArgLeuAlaProTrpThrPheAsnSerLeuArgLeuAs 799
    :||| :||| :||| :||| :||| :|||
1837 ----- 1837
    :||| :||| :||| :||| :||| :|||
799 pSerArgProProAlaArgLeuSerSerCysProThrValThrArgCysAlaProTrpLe 819
    :||| :||| :||| :||| :||| :|||

```

1838 -----GGGAGACCTTCACCCAGCAGCCTCGAGCGGTG 1869  
 819 uSerArgLeuProSerSerArgLeuSerSerArgProArgLeuThrSerArgProPr 839  
 1870 AAGA-----TCTCGCGG----- 1882  
 839 oArgLeuLeuSerValProLeuProLeuLeuSerArgLeuAlaArgSerArgAr 859  
 1883 -----TCAGAGACCTCATT 1896  
 859 gLeuAlaAlaGluAAsnLysProArgLeuSerMetAlaProLeuAlaThrThrSerAr 879  
 1897 TGGTCCCGGCGGCGGTGGAGATGTTATCGTATTCGCTTGGAGAGGATTCGAGGCC 1956  
 879 gSerPro-----ILSerLeuProProArgLeuSerArgLeuPr 893  
 1957 CAGCGGGCGCGAGTCA---TTGCCGTCTTAAAGCCGAGAGCTGACTC----- 2002  
 893 oThrArgAlaSerThrArgLeuProGluThrSerProSerProArgLeuThrSerAlaTr 913  
 2003 -----CGCATGGGTGCTGTGG---ATGCTGCCGTGGTGGCAAGGACACTGTT 2049  
 913 pAlaLeuThrArgValAspCysTrpLeuProSerArgProCysTrpProLeuSerSerVa 933  
 2050 GTGTGCACCTTTGAAATGAAACACAGAGTGTGCTGCGCGCTCGAGGGGTGGGC 2109  
 933 lAlaAlaProThrSerArgSerPheArgProIleThrTrpProArgLeuSerArgSe 953  
 2110 GCGAGGAGTTCGACATTTTACAGCTCTACGAGAGCTGGCGCGCTGGAGGCTGC 2169  
 953 rProArgValLeuThrThrAlaArgSerArgLeuCysAsnArgProSerTrpArgLeuSe 973  
 2170 A 2170  
 973 r 973

LT 10  
 19-252-991A-31760  
 Sequence 31760, Application US/09252991A  
 Invent No. 6551795  
 SERIAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 31760  
 LENGTH: 1706  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 19-252-991A-31760

iment Scores:  
 i. No.: 2,02e-11 Length: 1706  
 e: 258.00 Matches: 201  
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 : Local Similarity: 25.44% Mismatches: 259  
 y Match: 6.36% Indels: 273  
 4 Gaps: 43

19-836-392-8\_COPY\_22\_2205 (1-2184) x US-09-252-991A-31760 (1-1706)  
 3 GCTGAGGACCTCGCGGGCCACCGATGCCATGAAGAACTTCTCCAGTTCGCGGAGGAGGC 62  
 1088 AlaArgAlaProAla---HisArg-----Pro 1095

QY 63 CAGCATGTGTGCACCGGTGTGAGCACCCCTGCATCGTGGCGCTCATCGGCATCAG----- 116  
 Db 1096 GlnArgProAlaProProAlaLeuProAlaThrArgArgLeuGlnArgAspArgArg 1115  
 QY 117 ---CATCCACCCGCT-----CTGCTTCGCCCT 140  
 Db 1116 ValHisProLeuAlaGlyLeuValArgArgThrArgArgArgArgArgLeuArgPro 1135  
 QY 141 GGAGCTCCGCGCGCTCAGCAGCCTCAACACCGCTGCTGTCGAGAACGCCAGAGATTCTTC 200  
 Db 1136 ArgLeuArg---HisArgGluProGlyHisArgProLeuArgHisArgHisArgMetArg 1154  
 QY 201 CTTTATACCCCT-----GGGACACATGCTCACCACCAAAATAGCCTACCAGATCGC 251  
 Db 1155 ArgProLeuProProAlaAlaGlyThrArgProArgProGlyAsnLeuAlaThrLeuGly 1174  
 QY 252 CTCGGCGCTGCCCTACTCTGCACAGAGAAAACATCATCTTCTGACCTGAAGTCGACAA 311  
 Db 1175 AlaAlaAlaGlyAspProAla-----ProProGlyPhe 1186  
 QY 312 CATCTGTGTGTGCTCCCTTGAGTCAA----- 338  
 Db 1187 LeuProGlyLeuValProArgArgArgGlnArgThrArgThrAlaAlaArgArgHisArg 1206  
 QY 339 -----GGAGCACATCAACATCAAGCTATCTGACTACGGGATTCGAGGCGCATCATT 389  
 Db 1207 GluGlyProGlyAlaGlnArg----- 1213  
 QY 390 CCAATGAGGCGCCCTAGCGGTGGAGGCACTCTCTGGCTACCA-----GGCCCCAGAGAT 443  
 Db 1214 -----GlyAsnProSerHisGlySerSerGlyLeuProMetSerGlyProLys-Va 1231  
 QY 444 CAGGCGCTCGCATTTATATGATGAGAGGTAGATATGTTCTCTATGGAATGTGCTCTA 503  
 Db 1231 l---ValArgIleValThrArgGluGluAla-lleAlaThr----- 1243  
 QY 504 CGAGTTGCTGTGAG-----GACGCGCCCTG---CACTGGCGCCACCA 542  
 Db 1244 -----CysGluArgAspLeuGlnArgLeuAspLysAlaLeuAlaArgTrpGluAsnG 1261  
 QY 543 CCAGCTCCAGATTGCCAGA-----AGCTGTCCAGGGCATCCGCCGCTTCTGGGGCA 596  
 Db 1261 InAlaSerArgLeuAlaGlnLeuSerAspAlaGluArgAlaAlaAlaHis----- 1277  
 QY 597 GCGGAGGAAGTGCAGTTCGCGGCTGAGGCGCTCATGATGAGTGTGGGACACTAA 656  
 Db 1278 --AlaArgArgAlaSerLeuHisAlaLeuAlaArgThrGlyThrLeuAlaGlyArgAlaT 1297  
 QY 657 GCCAGAGAAGCGACCGCTGGCCCTGTCGTTGCGTGGTGGAGCCAGATGAAGGACCCGACTTTC 716  
 Db 1297 hrThrGlyGluAspArg-----LysArgIleP 1306  
 QY 717 CACCTTCATGTATGAACATGTGCTGGGAGACAGACAGCCCTTCTCTCATCCAGGGCCA 776  
 Db 1306 roGlnAlaArgProArgArgThrArgArgAlaArgHisProProGlyArgGlyLeThrP 1326  
 QY 777 GGAGTACACCGCTGTGTTTGGGATGGAAGAGG---AGTCCAGGAACCTACACGTTGT 833  
 Db 1326 roAlaThrProProProGlyLysArgGlnArgProAlaProGly----- 1341  
 QY 834 GAACACAGAGAAGCGCTCATGGAGGTGCAGAGATGCTGCTGGGATGAGGTGAG 893  
 Db 1342 --ProArgArgGlnAlaArgCysArgGlnArgGlySerProAla-----AsnProA 1358  
 QY 894 CTGCAGCTCCAGGTCAGAGATCCCTGTGGACAGCCAGGAGGACAGAAAATCTACAT 953  
 Db 1358 laSerAlaGlyArgArgArg-----ProProArgArgArgGlySerProA 1373  
 QY 954 CTACACCTCAAGGCGATGTGCCCTTAAACACACCCCAAGGCGCTTGGATCTCAGC 1013  
 Db 1373 laArgPro---ArgPheCysArgProArgGlnArgProArgArg----- 1386  
 QY 1014 TGTGCTCACCTGCTTCTTGGCGGTGCTGTTATTAATAAAGAAATTCCTACCTGCTTAGC 1073

1386 ----- 1386  
1074 GGGCTCGCGATGGCTGTGGTGTGTTCCCGTGGTGGCGGACCCCAAGACAG 1133  
1387 -----GlyThrProGlnArgSerP 1393  
1134 CTGCTCTACCTGTGTCACACACAGCCACAGGTCCAAAGTTCAGCATCGCGATGAAGA 1193  
1393 roAlaArgThr-----ArgProAlaProGluAspArgAsnAlaHisH1ProGlyT 1411  
1194 CGCAGCGGACACCTTACCAGTGAAGCCATGAGAGTGTCAACAGCGCT----- 1246  
1411 hrValAlaArgProAlaThrGlyArgProAlaArgThrAlaProGlyAlaHisArgP 1431  
1247 -----CTGAGGTCTGTGTCAGCAATGGCGCGCGCTCTGTCATCGACTGTGCTC 1298  
1431 roAlaHisArgThrAlaThrAlaAlaArgArg----- 1442  
1299 CTGGAGATCTGACGCGCTGGAGCCCTACATGGCCCTCCATGTTAGTCAGTCGT 1358  
1443 -----GlyGlnArgProSerValPro----- 1449  
1359 GTGACGCTCTGAGGCGAGGAGGAGTGTCTGTCGTCGTGATGACAGGCCAACTC 1418  
1450 -----ArgAlaThrGlyThrArgArgSer-----ArgThrAlaP 1461  
1419 CTGCTGTATGATACCTCCACCTCCACCTACCAGCTGTGTCCTCGT----- 1462  
1461 ro-----GlyAlaProGlnProAlaAlaArgGlnProGlyProArgProArgProG 1478  
1463 -----ACTTCTGGGGTCCCGAGCCCTCAGGACATGTTCCCGTGGCGGCC 1511  
1478 lyArgProArgThrProAlaAlaThrProAlaPro---GlyThr-----ProAlaArgP 1495  
1512 CT-----TGGACAGGAACCCCGGACCCAGCCAGCCAGCCAGCCAAAGTGCCTGA 1565  
1495 roArgGlnArgSerArgProArgArgArgArgThrArgArgThrAlaProAlaArgA 1515  
1566 GGGGACTCATCGCGAGTGTAGCATGATGATGAGTGTGAGAGTGGCGCAGATCCT 1625  
1515 rgArgLeuProAlaArgGlnArgSerAlaAlaThrArgArgThrHisArg----- 1531  
1626 GATCCACCGAGTACTCAGTACTGCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCT 1685  
1532 --AlaMetGlnArgHisProHisArgProProProAlaThrGlyArgProArgProP 1551  
1686 CGCCAGGCTGCCAGTCCCTCTCAA-----GCCTCCCA----- 1720  
1551 roGlyArgAlaProGlyProArgGlnProArgLeuArgSerProArgHisGlyHisA 1571  
1721 -----GCTCCCGAGCAAGTCTTCAGTGTGCTTCTCCACCGACTCGGAGACTC 1772  
1571 rgLeuGlyAlaAspArgGlnGlyArgPro-----AlaGlnThr- 1593  
1773 AGACATCTACATACGCGCGTCTGCTCTCCGACAGGTCTGAGCATGACCTGACCCCAT 1832  
1584 ArgHisProArg-----LeuArg-----ProGlySerArg 1593  
1833 GGAGCGGAGACCTTACGACAGCACTCGAGCGCGTGAAGATCTTCGCGGTCTCAG---AGA 1889  
1594 ArgGlnGlyArgGlnArgProProAlaThrAlaAlaArgArgProGlnArgGlnProArg 1613  
1890 CCTATTGGTCTCCAGCGCGGTGGAGATGTTATGCTCATTGCTGGAGGAGGATTC 1949  
1614 GlnProAlaArgProArgHisArgAsnProLeuValArgValPro----- 1629  
1950 TGAAGCCAGCGGCGCGAGTCTAT-----TGCGGTCTT 1982  
1630 ---ThrProProGlyProAlaAlaArgProGlyArgArgThrGlnArgGlyThrArgAla 1648  
1983 AAAGCCCGAGAGCT-----GACTCCGCA 2006

1649 GlyGlyGlyArgSerGlyValGluGlyAspTrpArgGlyArgAlaAlaGlyAspGlyGly 1668  
2007 TGGGCTGTGTGTGATCTCCGCTGTGTGGTGGCAAGGACACTGTTGTGTGACCTTTGAAA 2066  
1669 GlyAlaAlaGluGlyValValGlyGlyProAlaGlyAlaSerAlaArgHisSerIleArg 1688  
2067 TGAACAACACAGAGTGTGCTGCTGGC 2090  
1689 AlaValHisArgLeuThrProGly 1696  
RESULT 11  
US-09-345-473E-43  
; Sequence 43, Application US/09345473E  
; Patent No. 6558903  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin  
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
; FILE REFERENCE: 35800/183781  
; CURRENT APPLICATION NUMBER: US/09/345,473E  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 626  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-345-473E-43  
Alignment Scores:  
Pred. No.: 2,13E-11 Length: 626  
Score: 255.50 Matches: 150  
Percent Similarity: 33.59% Conservative: 71  
Best Local Similarity: 22.87% Mismatches: 242  
Query Match: 6.30% Indels: 193  
Gaps: 28  
US-09-836-392-8\_COPY\_22\_2205 (1-2184) x US-09-345-473E-43 (1-626)  
QY 4 CTGAGGCACCTGCGGGCCAGCCGATGCCATG-----AAGAAC 39  
DB 74 ValArgHisArgGlnSerGlyGlnValMetValLeuLysMetAsnLysLeuProSerAsn 93  
QY 40 TTCTCCGAGTTCGGGACGAGGAGCCAGCATGTCGCGGCTGCGAGCACCCTGCTGCTG 99  
DB 94 ArgGlyAsnThrLeuArgGluValGlnLeuMetAsnArgLeuArgHisProAsnIleLeu 113  
QY 100 GCGCTCATCGGCATCAGCATCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 159  
DB 114 ArgPheMetGlyValCysValHisGln-----GlyGlnLeuHis 126  
QY 160 AGCCTCAACACCGCTGCTGCTGCGAGAACGCCAGAGAT-----TCTTCTTTTATACCC 210  
DB 127 AlaLeuThrGluTyrMetAsnGlyGlyThrLeuGluGlnLeuLeuSerSerProGluPro 146  
QY 211 CTGGGACATGCTCACCACCAAAATAGCTACCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 270  
DB 147 LeuSerTrpProValArgLeuHisLeuAlaLeuAspIleAlaArgGlyLeuArgTyrLeu 166  
QY 271 CACAAGAAACATCATCTTCTGACCTGAAGTCCGACCAACATCTCTGCTGCTGCTGCTGCT 330  
DB 167 HisSerLysGlyValPheHisArgAspLeuThrSerLysAsnCysLeuValArgArgGlu 186  
QY 331 GACGTCAAGGACACATCAACATCAAGCTATCTACTACGAGGATTCGAGGCAG----- 384  
DB 187 Asp-----ArgGlyPheThrAlaValValGlyAspPheGlyLeuAlaGluLysIlePro 204  
QY 385 TCATTCATCATGAGGCGCC-----CTAGCGCTGGAGGCGACTCTCTGCTGCTGCTGCTGCT 432  
DB 205 ValTyrArgGluGlyAlaArgLysGluProLeuAlaValValGlySerProTyrTrpMet 224  
QY 433 GCGCCAGAGATCAGCGCTCGCATTTGATATATATGATGAGAGGTAGATATGTTCTCTATGGA 492  
DB 225 AlaProGluValLeuArgGlyGluLeuTyrAspGluLysAlaAspValPheAlaPheGly 244

493 ATGTGCTCTACGAGTTCGTGCA-----GGACAGCGCCCTGCACGTG 534  
:::||||| |||||:::|  
245 IleValLeuCysGluLeuIleAlaArgValProAlaAspProAspTyrLeuProArgThr 264  
:::|:::|:::|:::|:::|  
535 GGCCACCACCAGCTCCAGATTCAGATTCGCCAAGAAGTGTCCAAAGGCATCCGCCGCTTCTGGGG 594  
:::|:::|:::|:::|:::|  
265 GluAspPheGlyLeuAspVal-----ProAlaPheArgThrLeuValGly 279  
:::|:::|:::|:::|:::|  
595 CAGCCGAGGAAGTGCAGTTTCGCGGACGTGCAGGCGCTCATGATGGATGTGTGGACACT 654  
:::|:::|:::|:::|:::|  
280 AspAspCysProLeuProPhe-----LeuLeuLeuAlaIleHisCysCysAsnLeu 296  
:::|:::|:::|:::|:::|  
655 AAGCCAGAGAAGCGACCGCTGGCCCTGCTCG-----GTGCTGAGC 693  
:::|:::|:::|:::|:::|  
297 GluProSerThrArgAlaProPheThrGluIleThrGlnHisLeuGluTrpIleLeuGlu 316  
:::|:::|:::|:::|:::|  
694 CAGATGAGGACCCGACTTTTGGCACTTCATGTATGAACACTGCTGTGTGGGAACGACACA 753  
||:::|:::|:::|:::|:::|  
317 GlnLeuProGluProAlaProLeuThr-----ArgThr 327  
||:::|:::|:::|:::|:::|  
754 GCCTCTCTCTCATCCAGGCGCAGGAGTACACGTGGTGTCTTTGGATGGAAAGAGGAG 813  
|||:::|:::|:::|:::|:::|  
328 AlaLeuThrHisasnGlnGly--SerValAlaArgGly----- 339  
|||:::|:::|:::|:::|:::|  
814 TCCAGGAACCTACACGGTGTGTGAACACAGAGAAGGCGCTCATGAGGTGCAGAGGATGTC 873  
|||:::|:::|:::|:::|:::|  
340 -----GlyPro----- 341  
|||:::|:::|:::|:::|:::|  
874 TGCCCTGGGATGAAGGTGAGCTGCCAGCTCCAGGTCACAGATCCCTGTGCACAGCCACC 933  
|||:::|:::|:::|:::|:::|  
342 -----SerAlaThrLeuProArgProAspProArgLeu-----SerA 354  
|||:::|:::|:::|:::|:::|  
934 GAGGACCCAGAAATCTACATCTACACCCCTCAA----- 965  
|||:::|:::|:::|:::|:::|  
354 rgSerArgSerAspLeuPheLeuProProSerProGluSerProProAsnTrpGlyAspA 374  
|||:::|:::|:::|:::|:::|  
966 -----CGGCATGTGCCCC 978  
|||:::|:::|:::|:::|:::|  
374 snLeuThrArgValAsnProPheSerLeuArgGluAspLeuArgGlyGlyIleLeuLysL 394  
|||:::|:::|:::|:::|:::|  
979 TTAACACACCCCAACAGGCGCTTGGATATCTCCAGCTGTGCTCACCTGCTTCTGTGGCCGTG 1038  
|||:::|:::|:::|:::|:::|  
394 euLeuAspThrProSer--LysProValLeuProLeuValProProSerProPheProSe 413  
|||:::|:::|:::|:::|:::|  
1039 CCTGTTATTAAAGAATCTCACTGCTTCTAGCGGCGCTCCGCATGGCGCTTGTGGCT 1098  
|||:::|:::|:::|:::|:::|  
413 rThrGlnLeuProLeuValThrThrProGluThrLeuValGlnPro----- 428  
|||:::|:::|:::|:::|:::|  
1099 GTGTTTCCGCTGTGCGGGCGCACCCCAAGG-----ACAGCTGCTCCTAC 1143  
|||:::|:::|:::|:::|:::|  
429 -----GlyThrProAlaArgCysArgSerLeuProSerSerProG 443  
|||:::|:::|:::|:::|:::|  
1144 CTGTGCTCACACACCCCAACA-----GTCCAAAG 1173  
|||:::|:::|:::|:::|:::|  
443 uLeuProArgArgMetGluThrAlaLeuProGlyProGlyProProAlaValGlyProSe 463  
|||:::|:::|:::|:::|:::|  
1174 TTCAGATCGCGGATCAAGACGACAGCGACAGACCCCTACCCAGTGAAGCCATCGAGGTG 1233  
|||:::|:::|:::|:::|:::|  
463 rAlaGluGluLysMetGluCysGluGlySerSerProGluProGluProGlyProAl 483  
|||:::|:::|:::|:::|:::|  
234 GTCACAGCGGCTCTGAGTCTGGTATGACCAATAGGCGCGGCGCTCTTGTCTCATCGACTGT 1293  
|||:::|:::|:::|:::|:::|  
483 aProGlnLeuProLeuAlaValAlaThrAspAsnPheIleSerThrCysSerSerAlaSe 503  
|||:::|:::|:::|:::|:::|  
1294 GCCTCCCTGG----- 1303  
|||:::|:::|:::|:::|:::|  
503 rGlnProTrpSerProArgSerGlyProValLeuAsnAsnAsnProProAlaValValVa 523  
|||:::|:::|:::|:::|:::|  
1304 -AGATTCGACGGCGGTGAGCGCCTACATGCGCCCTCCATGGTTTACGTTCAGTGTGCTGTC 1362  
|||:::|:::|:::|:::|:::|  
523 lAsnSerProGlnGlyTrpAla-----GlvGluProTrpAsnArgAlaGlnHisSe 540  
|||:::|:::|:::|:::|:::|

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QY 1363 AGCTCTGAGGCGACAGGGGAGGAGGTGCTGTGTGCTGGATGACAAAGCCAACTCTTTG 1422
Db : |||||
540 rLeuProArgAla-----AlaAlaLeuGluArgThrGluPro-- 552
      |||||
QY 1423 GTGATGTACACTCCACCACCTACCAGCTGTGTGCCGGTACTTCTGCGGGGTCGCCAGC 1482
Db : |||||
553 -----SerProProSerAlaProArgGluProAspGluGlyLeuProCy 568
      |||||
QY 1483 CCCTCAGGACATGTTCCCGTCGCGCCCTTGGACACGGAAACCCCGGAGCCAGCCAC 1542
Db : |||||
568 sPro--GlyCysCysLeu-----GlyProPheSerPheGlyPheLeuSerMetCysPr 585
      |||||
QY 1543 ACGGCCAACCAAGGTGCTGTAGGGGACTCCATCGCGACGTGAGCATCATGTACAGT 1602
Db : |||||
585 oArgProThrProAlaValalaArgTyrArgAsn-----LeuAsnCysGluAl 601
      |||||
QY 1603 GAGGAGTGGGCACGAGATCCTGTATCCACCAGGAATCACTCACTACTGCTCCATG 1662
Db : |||||
601 aGlySerLeuLeu-----CysHisArgGlyHisHisAlaLys----- 613
      |||||
QY 1663 TCCTCTACTCTTCATCCCAACCCCGCAGGTCGCCAGGT 1702
Db : |||||
614 -ProProThrPro-----SerLeuGlnLeuProGly 623

RESULT 12
US-09-252-991A-24567
; Sequence 24567 Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24567
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24567

Alignment Scores:
Pred. No.: 3 41e-11 Length: 681
Score: 253.00 Matches: 210
Percent Similarity: 29.96% Conservative: 30
Best Local Similarity: 26.22% Mismatches: 232
Query Match: 6.21% Indels: 332
DB: 4 Gaps: 54

US-09-836-392-8_COPY_22_2205 (1-2184) x US-09-252-991A-24567 (1-681)
QY 1840 CCCGTCATAGG-----GGTCCAGTCATGCTCAGACTGTGCGAGGCAG----- 1796
Db 9 ProProProTriAlaCysAsnSerThrGlyArgThrProThrAspGlyArgSerGlySer 28
      |||||
QY 1795 ---CACGGCGGTATGATGATGCTCTGACT-----CCTGCAGCT 1760
      |||||
Db 29 ThrArgArgSerSerAlaAlaCysTrpLysHisSerAlaIleArgArgValArgAsn 48
      |||||
QY 1759 CGGTGAGAAAGCACACTGGAGAACTTGTCTGGGAGCTGGGGAGCTTGAGGGGAC 1700
      |||||
Db 49 ArgSerAsnArgAla--TrpProArg-----TrpProGlyCysAlaArgThr 63
      |||||
QY 1699 -----TGGCAGCTGCGCGGGTGGGATGAGGAGTAGGAGGACATCG 1658
      |||||
Db 64 AlaProThrSerAspCysTrpSerAlaAsnAlaSerArgTrpSerLysArg----- 81
      |||||
QY 1657 AGCAGTAGTCAGTCACTGATTCCTGCTGTGATCAGGATCTGCGTGCCAGCTCCTCACTGT 1598
      |||||

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> 9-345-473E-48
> sequence 48, Application US/09345473E
> cont No. 6558903
> LOCAL INFORMATION:
> APPLICANT: Hodges, Martin
> TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
> FILE REFERENCE: 35800/183781
> CURRENT APPLICATION NUMBER: US/09/345,473E
> CURRENT FILING DATE: 1999-06-30
> NUMBER OF SEQ ID NOS: 62
> SOFTWARE: FastSeq for Windows Version 4.0
> Q ID NO 48
> LENGTH: 628
> TYPE: PR1
> ORGANISM: Rattus norvegicus
> 9-345-473E-48

> Alignment Scores:
> e. No.: 3,948-11 Length: 628
> e: 252.00 Matches: 153
> e: 35.56% Conservative: 71
> e: 24.29% Mismatches: 272
> e: 6.21% Indels: 134
> e: 4 Gaps: 26

> 9-836-392-8_COPY_22_2205 (1-2184) x US-09-345-473E-48 (1-628)
> 4 CTGAGGCGACCTCGGGCCACCGATGCCATG-----AAGAAC 39
> 69 ValArgHisArgGlnSerGlyGlnValMetValLeuLysMetAsnLysLeuProSerAsn 88
> 40 TTCCTCGAGTTCGGCAGAGCCAGCATGTCGACGGCTGCGAGCCGCTGCGATCGTGG 99
> 89 ArgSerAsnThrLeuArgGluValGlnLeuMetAsnArgLeuArgHisProAsnIleLeu 108
> 100 GCGCTCATCGGATCAGATCACCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 159
> 109 ArgPheMetGlyValCysValHisGln-----GlyGlnLeuHis 121
> 160 AGCTTCAACACCGTCTCTCGAGAACGCCAGAGAT-----TCTTCTTTTATACCC 210
> 122 AlaLeuThrGluTyrMetAsnGlyGlyThrLeuGluGlnLeuLeuSerSerProGluPro 141
> 211 CTGGGACACATGCTCACCCAAAATAGCTACAGATCGCTCGGCTGCGCTGCTGCTGCTG 270
> 142 LeuSerTrpProValArgLeuHisLeuAlaLeuAspIleAlaGlnGlyLeuArgTyrLeu 161
> 271 CACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACACATCTGTGTGTGCTGCTT 330
> 162 HisAlaLysGlyValPheHisArgAspLeuThrSerLysAsnCysLeuValArgArgGlu 181
> 331 GAGCTCAAGGACCATCAACATCATAGTATCTGACTACGGGATTCGAGGAG-----384
> 182 Asp-----GlyGlyPheThrAlaValValGlyAspPheGlyLeuAlaGluLysIlePro 199
> 385 TCATTCCATAGCGGGCC-----CTAGCGCTGGAGGCGACTCTCTGCTTACCCAG 432
> 200 ValTyrArgGluGlyAlaArgLysGluProLeuAlaValValGlySerProTyrTrpMet 219
> 433 GCCCAGAGATCAGCGCTCGCATTTATATATATATATATATATATATATATATATATATAT 492
> 220 AlaProGluValLeuArgGlyGluLeuTyrAspGluLysAlaAspValPheAlaPheGly 239
> 493 ATGGTGCTCTAGCTTCTGTCA-----GGACAGCGCTGCTGCTGCTGCTGCTGCTGCTG 534
> 240 IleValLeuCysGluLeuIleAlaArgValProAlaAspProAspTyrLeuProArgThr 259
> 535 GCCCACCACCATCGATCCAGATGCCAAGAGCTGTCCAAGGGCATCCCGCGCTTCTGGGG 594
> 260 GluAspPheGlyLeuAspVal-----ProAlaPheArgThrLeuValGly 274

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QY 595 CAGCCGGAGGAGTGCAGTTCCGCGCAGCTGCAGGCGCTCATGTGGAGTCTCTGGGACACT 654
Db 275 AsnAspCysProLeuProPhe-----LeuLeuLeuAlaIleHisCysCysSerMet 291
QY 655 AAGCCAGAGAGCGACCGCTGGCGCTGTCGTTGGTGGAGCCAGATGAAGGACCCGACTTTT 714
Db 292 GluProSerAlaArgAlaProPheThrGluIleThrGlnHisLeuGluGln-----308
QY 715 GCCACCTTCATGTATGAACCTGTGTGTGGGAAGCAGACAGCCCTTCTTCATCCCAAGGCG 774
Db 309 -----IleLeuGlu--GlnLeuProGluProThrProLeuAlaLysMetPro-----323
QY 775 CAGAGTACACCGCTGCTGTTTGGATGGAAAAGAGAGATCCAGGAACACTACCGGTGGTG 834
Db 324 -----LeuAlaLysAlaProLeuThrTyrAsnGlnGly-----334
QY 835 AACACAGAGAAGGCGCTCATGGAGTGCAGAGGATGTGTGCTGCTGGATGAAGGTGAGC 894
Db 335 -----SerValProArgGlyGlyProSerAlaThrLeuProArgSerAspProArgL 352
QY 895 TGCCA-----GCTCCAGTCCAGAGATCCCTGTGGAC-----926
Db 352 euserArgSerArgSerAspLeuPheLeuProSerProGluSerProProSerTrpG 372
QY 927 -----AGCCACCGAGGACCGAGAAATCTACATCTACACCCCTCAAGGCG-----969
Db 372 LyAspAsnLeuThrArgValAsnProPheSerLeuArg--GluAspLeuArgGlyGlyLys 391
QY 970 -----ATGTGCCCTTTAAACACACACCCCAA 993
Db 392 IleLysLeuLeuAspThrProCysLysProAlaThrProLeuProLeuValProSer 411
QY 994 CAGCCCTTGATCTCCAGCTGTCGTCACCTGCTTCTTGGCGTGGCTGCTTATTATAAAG 1053
Db 412 ProLeuThrSerThr--GlnLeuProLeuValAlaSerProGluSerLeuValGlnProGl 431
QY 1054 AATTCCTACCTGCTTAGCGGCGCTCGCGATGGCTGTGTGTGCTGCTGCTTTCCTCGGTG 1113
Db 431 uThrProValArgArgCysArgSerLeuProSerSerProGluLeu-----446
QY 1114 CGGGGACCCCAAGG-----ACAGTGTCTCTACTGTGTCTACACACAGCAACAGG 1167
Db 447 -----ProArgArgMetGluThrAlaLeuProGly---ProGlyProSerProValGl 463
QY 1168 TCCAAGTTCAGCATCGCGATGAAGCGCAGCAGCAACCCCTACCCAGTGAAGGCGCATG 1227
Db 463 yProSerThrGluGluArgMetAspCysGluGlySerSerProGluProGluProGl 483
QY 1228 GAGGTGTCAACAGCGCTCTGAGGTCTGGTACCAATGGCGCGGCTCTCTGTGTCTC 1287
Db 483 yProAlaProGlnLeuProLeuAlaValAlaThrAspAsnPheIleSerThrCysSerSe 503
QY 1288 GACTGTGCTCTCGGAGATCTGACGCGCTGAGCCCTACATGGCCCTCCCA-----1342
Db 503 fAlaSerGlnProTrpSerAlaArgProGlyProSerLeuAsnAsnAsnProAlaVa 523
QY 1343 -----TGGTTACGTACGTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 523 lValValAsnSerProGlnGlyTrpAlaArgGluProTrpAsnArgAlaGlnHisSerLe 543
QY 1381 GAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Db 543 uProArgAlaAlaAlaLeuGluArgThrGluProSer-----Pr 556
QY 1441 ACCTACAGAGTGTGTGCGGCTACTTCTGCGGCGTCCCGAGCCCTCAGGACATGTTT 1500
Db 556 oProSerAlaProArgGluGlnGluGluGlyLeuProCysPro--GlyCysCysLe 575
QY 1501 CCCGTGCGGCGCTTGGACAGCGAACCCCGCGGAGCCAGCCACACGCGCCCAACCCAAAGGTG 1560
Db 575 u-----SerProPheSerPheGlyPheLeuSerMetCysProArgProThrProAlaVa 593
QY 1561 CCTGAGGGGAGCTCCATCGCGGAGCTGAGCATCATGTACAGTGAGGAGCTGGCGCAGCAG 1620

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1300 CTGAGATGTCAGGCGGTGGAGCCCTCATATGCGCCCTCCATGTTACGTCACTGTC 1359  
 481 oserHisThrAspGly----- 486  
 1360 TGCAGCTCTGAGGCGAGGAGGAGGAGGTCGTCTGTCCTGGATGACAGGCCAACTCC 1419  
 487 -----AlaMetLeuAlaArgLysLeuSerLeuGlyGlyGly-----ArgPro----- 500  
 1420 TTGGTGATGATPACCATCCACCATCTACCATGCTGTGTCGCGGTACTTCTGCGGGTCC 1479  
 501 -----TyrThrProSerProGlnValGlyThrIleProGluArgProSerTyrSerAr 518  
 1480 AGCCCTCTCAGGACATGTTCCGTCGCGCCCTTGGACAGGAACCCCGGAGCCAGC 1539  
 518 gValProSer-----ProGlnGlyAlaAspValArgValGlyArgSerPro-- 533  
 1540 CACACGCCCAACCAAGGTGCTCGAGGGGACTCATCGCGGAGCTGAGCATCATGTAC 1599  
 534 ----ArgProGlySerSerValProGluHisSerProArgThrThrGlyLeuGlyCys-- 551  
 1600 AGTGAGAGCTGGGACCGAGATCCTGTATCCACAGGAATCACTCACTGACTACTGCTCC 1659  
 552 -----ArgLeuHisSer-----AlaPr 557  
 1660 ATGTCTCTCTCTCTATCCATCCACCCGCGAGGCTGCGAGGTCCCTCAAGCCTCCCC 1719  
 557 oAnLeuSerAspPheHisValValArgProLysLeuProLysPro----- 572  
 1720 AGTCCCTCCAGCAAGTTCCTCCAGTGTGCTTTCTCCACCG---ACTGGAGGACTCAGAC 1776  
 573 ----ProThrAspProLeuGlyAlaThrPheSerProProGlnThrSerAlaProGlnPr 591  
 1777 ATGCTACATACGCCCGGTCTGCTCCCGACAGGTCTGAGCATGACCTGACCCCATGGAC 1836  
 591 oCys----- 592  
 1837 GGGGAGACCTTCAGCAGCAGCCTGAGGCGGTGAAGATCCTCGCGG----- 1882  
 593 -----ProGlyLeuGlnSerCysArgProLeuArgGlySerProLysLeuProAspPh 610  
 1883 -----TCAGACACCTCATTTGG----- 1900  
 610 eLeuGlnArgSerProLeuProProIleLeuGlySerProThrLysAlaGlyProSerPh 630  
 1901 -----TCCCGAGGCGCGGTGAGATGTTATCGTCATTGGCTGGAGAAG-- 1945  
 630 eAspPheProLysThrProSerSerGlnAsnLeuLeuThrLeuLeuAlaArgGlnGlyVa 650  
 1946 -ATTCTGAAGCCCGAGGCGGCGAGTCAATGCGCTTTAAAGCCCGAGAGCTGACTCCG 2004  
 650 lValMetThrProProArgAsnArgThrLeuProAspLeuSerGluAlaSer----- 667  
 2005 CATGGGGTCTGTGTGATGCTCCGCTGTTGCCAAGGACACTGTTGTGCACCTTTGAA 2064  
 668 -----ProPheHisGlyGlnLeu----- 674  
 2065 AATGAAACACAGATGTTGCTGCGCTCTGGAGGGGCTGGGCGGCGAGGAGTTCGAC 2124  
 675 -----GlySerGlyLeuArgProAlaGluAspThrArgGlyProPheGlyArgSe 691  
 2125 ATTCTTACCACT 2137  
 691 rPheSerThrSer 695

LT 15  
 19-266-225D-12  
 Sequence 12, Application US/09266225D  
 Patent No. 6573364  
 SERIAL INFORMATION:  
 APPLICANT: Nandabalan, Krishan  
 APPLICANT: Kingmore, Stephen  
 APPLICANT: Tchernev, Velizar  
 TITLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak

TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein-  
 TITLE OF INVENTION: Interacting Proteins  
 FILE REFERENCE: 15966-523  
 CURRENT APPLICATION NUMBER: US/09/266,225D  
 CURRENT FILING DATE: 1999-03-10  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 12  
 LENGTH: 816  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-266-225D-12

Alignment Scores:  
 Pred. No.: 1.63e-10 Length: 816  
 Score: 244.50 Matches: 170  
 Percent Similarity: 34.47% Conservative: 82  
 Best Local Similarity: 23.26% Mismatches: 252  
 Query Match: 6.03% Indels: 227  
 DB: 4 Gaps: 36

US-09-836-392-8\_COPY\_22\_2205 (1-2184) x US-09-266-225D-12 (1-816)

QY 19 GCACCGATGTCATGAAGAACTTCTCCAGTTCGGAGGAGGCCAGCATGCTGCACGCG 78  
 DB 89 AlapheAspValValThrAspAlaLysArgThrLeuArgGluLeuLysHis 108  
 QY 79 CTGACGACCCCTGATCGTGGCGCTCATCGCATCAGCATCCACCCTGCTGC----- 132  
 DB 109 PheLysHisAspAsnIleAlaIleLysAspIle-----LeuArgProThrValProTyr 127  
 QY 133 -----TTGCGCCTGGAGCTGCGCGCTCAGCAGCCTCAACCCGCTGCTCGGAGAAC 186  
 DB 128 GlyGluPheLysSerValTyrValValLeuAspLeuMetGluSerAspLeuHisGln 147  
 QY 187 GCAGAGATTTCTCTTATACCTCGGACACATGCTCACCAAAAAATAGCTACACAG 246  
 DB 148 IleHisSerSerGlnProLeuThrLeuGluHisVal-----ArgTyrPheLeuTyrGln 165  
 QY 247 ATCGCCTCGGCGCTGCGCTACCTGCACAGAAACATCATCTTCTGTGACCTGAGAGTCG 306  
 DB 166 LeuLeuArgGlyLeuLysTyrMetHisSerAlaGlnValIleHisArgAspLeuLysPro 185  
 QY 307 GACACATTTCTGTGTGCTCCCTTGTGAGTCAAGGAGCAGCATCAACATCAAGCTATCTGAC 366  
 DB 186 SerAsnLeuLeu-----ValAsnGluAsnCysGluLeuLysIleGlyAsp 200  
 QY 367 TACGGATTTTCGAG-----CAGTCATTCCATGAGGCG 399  
 DB 201 PheGlyMetAlaArgGlyLeuCysThrSerProAlaGluHisGlnTyrPheMetThrGlu 220  
 QY 400 GCCCTAGCGTGGAGGCGACTCTGCGTACAGGCCCGCCAGAGATCAGGCCCTGCATTT--- 456  
 DB 221 TyrVal-----AlaThrArgTyrTyrArgAlaProGluLeuMetLeuSerLeuHis 237  
 QY 457 GTATATGATGAGAAGGTAGATATGTTCTCTTATGAGATGCTCTACGAGTTCTGTCTCA 516  
 DB 238 GluTyrThrGlnAlaIleAspLeuTyrSerValGlyCysIlePheGlyGluMetLeuAla 257  
 QY 517 GCACAGCGC-----CTGCACTGGGCCAC---CACAGCTCCAGATTGCCAAGAAGCTG 567  
 DB 258 ArgArgGlnLeuPheProGlyLysAsnTyrValHisGlnLeuGlnLeu----- 273  
 QY 568 TCCAGGCGCATCGCCGCTTCTGGGCGAGCG-----GAGGAAGTGCAG 612  
 DB 274 -----IleMetValLeuGlyThrProSerProAlaValIleGlnAlaValGly 290  
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GenCore version 5.1.1.6  
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Sequence 6, Appli  
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## ALIGNMENTS

### RESULT 1

US-09-836-392-21  
; Sequence 21, Application US/09836392  
; Patent No. US20020173458A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides, Antibodies  
; TITLE OF INVENTION: Antibodies  
; FILE REFERENCE: PTO20P1  
; CURRENT APPLICATION NUMBER: US/09/836,392  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: PCT/US00/28066  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: 60/159,542  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: 60/165,914  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/189,027  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 728  
; TYPE: PRT

ORGANISM: Homo sapiens

J9-836-392-21

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Publication No. US20030045699A1  
GENERAL INFORMATION:  
APPLICANT: WEISS, BERTRAM  
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS  
FILE REFERENCE: SCH-1811  
CURRENT APPLICATION NUMBER: US/10/132,382  
CURRENT FILING DATE: 2002-04-26  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 1987  
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0-132-382-6

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 1801 TCCGACAGGTCTGAGCATGACCTGACCCCTGAGCGGAGACCTTCAGCCAGCACCTG 1860  
 1861 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 1880  
 1861 CAGCGCGTGAAGATCTCCGCTCAGACCTCATTTGGTCCCGAGCGCGTGGAGAT 1920  
 1881 GlnAlaValIleLeuAlaValArgAspLeuIleTrpValProArgArgGlyGlyAsp 1900  
 1921 GTTATCGTCAATTGGCTGAGAGGATCTGAGCCCGAGCGGCGGAGTCAATTGCCGTC 1980  
 1901 ValIleValIleGlyLeuGluAspSerGlyAlaGlnArgGlyValIleAlaVal 1920  
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 1921 LeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaAlaValAlaLys 1940  
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 2101 GGTGGGGGGCCAGGAGTTCACATTTTACAGTCTACAGAGAGCTGGGCGGCGCTG 2160  
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 1981 GluAlaCysThrArgLysArg 1987

JLT 3  
 10-132-382-2  
 Sequence 2, Application US/10132382  
 Publication No. US20030045699A1  
 GENERAL INFORMATION:  
 APPLICANT: WEISS, BERTRAM  
 TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS  
 FILE REFERENCE: SCH-1811  
 CURRENT APPLICATION NUMBER: US/10/132,382  
 CURRENT FILING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2  
 LENGTH: 2013  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 10-132-382-2

Alignment Scores:  
 d. No.: 4,99e-215 Length: 2013  
 re: 3574.50 Matches: 687  
 t Local Similarity: 94.50% Conservative: 0  
 t Similarity: 94.50% Mismatches: 1  
 y Match: 88.09% Indels: 39  
 15 Gaps: 1

09-836-392-8\_COPY\_22\_2205 (1-2184) x US-10-132-382-2 (1-2013)

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 QY 121 CACCGCTCTCTTTCGCGCTGAGCTCGCGCCCTCAGCAGCTCAACACCGTCTGCTGCC 180  
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 QY 181 GAGAACGCGACAGATTTCTCTTATACCCCTGGACACATGCTCACCCCAAAATAAGCC 240  
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 QY 241 TACCAAGATCGGCTCGCGCTGAGCTCATCTGACCAAGAAACATCATCTTCTGTGACCTG 300  
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1967 AspThrValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArg 1986  
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2161 GAGGCTTGCACTCGCAAGAGA 2181

Db 2007 GluAlaCysThrArgLysArg 2013  
RESULT 4  
US-10-132-382-8  
; Sequence 8, Application US/10132382  
; Publication No. US20030045699A1  
; GENERAL INFORMATION:  
; APPLICANT: WEISS, BERTRAM  
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS  
; FILE REFERENCE: SCH-1811  
; CURRENT APPLICATION NUMBER: US/10/132.382  
; CURRENT FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 2014  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-132-382-8  
Alignment Scores:  
Pred. No.: 4,98e-215 Length: 2014  
Score: 3574.50 Matches: 687  
Percent Similarity: 94.50% Conservative: 0  
Best Local Similarity: 94.50% Mismatches: 1  
Query Match: 88.09% Indels: 39  
DB: 15 Gaps: 1  
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RESULT 6

US-10-094-749-1689  
 ; Sequence 1689, Application US/10094749  
 ; Publication No. US20030219741A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ISOGAI, TAKAO  
 ; APPLICANT: SUGIYAMA, TOMOYASU  
 ; APPLICANT: OTSUKI, TETSUJI  
 ; APPLICANT: WAKAMATSU, AI  
 ; APPLICANT: SATO, HIROYUKI  
 ; APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI

APPLICANT: ISONO, YUUKO

APPLICANT: HIO, YURI

APPLICANT: OTSUKA, KAORU

APPLICANT: NAGAI, KEIICHI

APPLICANT: IRIE, RYOTARO

APPLICANT: TAMECHIKI, ICHIRO

APPLICANT: SEKI, NAOHIKO

APPLICANT: YOSHIKAWA, TSUTOMU

APPLICANT: OTSUKA, MOTOKYUKI

APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

FILE REFERENCE: 084335/0160

CURRENT APPLICATION NUMBER: US/10/094,749

PRIORITY FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 60/350,435

PRIOR FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 3381

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1689

LENGTH: 501

TYPE: PRT

ORGANISM: Homo sapiens

10-094-749-1689

Invent Scores:

1. No.: 1,05e-155 Length: 501

Matches: 501

Conservative: 0

Mismatch: 0

Indels: 1

Gaps: 0

09-836-392-8\_COPY\_22\_2205 (1-2184) x US-10-094-749-1689 (1-501)

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261 TyrSerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGluIleCysArgArg 280

1318 CTGGAGCCCTACATGCGCCCTCTCATGTTACGTACGTGCTGTCAGCTCTGAGGCGAGA 1377

281 LeuGluProTyrMetAlaProSerMetValThrSerValValCysSerSerGluGlyArg 300

1378 GGGGAGGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437

301 GlyGluGluValValTyrCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSer 320

1438 ACCACTACAGCTGTGTGCGGCTCTTCTGCGGGTCTCCAGCCCTCCAGGACATG 1497

321 ThrThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMet 340

1498 TTTCCCGTGGCGCTTGGACACGGAACCCCGGCGACGACACACGCGCAACCCCAAG 1557

341 PheProValArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLys 360

1558 GTGCTGAGGGGAGCTCCATCCGCGAGCTGAGCATCATGACAGTGGAGGCTGGGACAG 1617

361 ValProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThr 380

1618 CAGATCCTGATCCACCGAATCACTCACTGCTACTGCTCTCTCTCTCTCTCTCTCTCTCA 1677

381 GlnIleLeuIleHisGlnGluSerLeuThrAspTyrCysSerMetSerTyrSerSer 400

1678 TCCCAACCCCGCGAGCTGCCAGGTCCCTCAAGCTCCCGAGCTCCCGAGCAAGTTCT 1737

401 SerProProArgGlnAlaAlaArgSerProSerSerLeuProSerProAlaSerSer 420

1738 TCAGTGTGCTTTCTCCACCGAGCTGCGAGGACCTCAGACATGCTACATACGCCCGGTGCT 1797

421 SerSerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAla 440

1798 GCTCCGACAGCTCTGAGCATGACCTGACCCCGATGAGCGGGGAGACCTTCAGCCAGCAC 1857

441 AlaSerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHis 460

1858 CTGAGCGCGTGAAGATCTCTCCCTGAGACCTCATTTGGTCTCCCGAGCGCGGTGGA 1917

461 LeuGlnAlaValIleLeuAlaValArgAspLeuIleTyrValProArgArg-ValGln 480

1918 GATGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1977

480 MetLeuSerSerLeuAlaTyrArgArgIleLeuLysProSerGlyAlaGluSerLeuPyr 500

1978 GTCT 1981

500 oSer 501

RESULT 7

US-10-143-133-2

; Sequence 2, Application US/1043133

; Publication No. US20020197658A1

GENERAL INFORMATION:  
 APPLICANT: Yoganathan, Thillainathan  
 APPLICANT: Delaney, Allen  
 TITLE OF INVENTION: Cancer Associated Protein Kinase and Its Use

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FILE REFERENCE: KINE-023
CURRENT APPLICATION NUMBER: US/10/143,133
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 60/290,555
PRIOR FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
Q ID NO 2
LENGTH: 847
TYPE: PRT
ORGANISM: Homo sapien
0-143-133-2
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e:	37.50
ent Similarity:	135
Local Similarity:	Conservative: 25
y Match:	Mismatches: 741
	Indels: 283
	Gaps: 38
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9-836-392-8 COPY 22 2205 (1-2184) x US-10-143-133-2 (1-847)

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112	ATCAGATCATCACCG-----CTCTGCTTCGGCCTCGAGCTCGCGCGCTCAGCAGCCTC	165
182	ValCysLeuGlnGluProAsnLeuCysLeuValMetGluTyRAlaAlaGlyGlyProLeu	201
166	ACACCGTGTCTCCGAGAACGCCAGAGATCTTCTTTATACCTCTGGGACACATGCTC	225
202	SerArgAlaLeuAlaGlyArgArg-----ValPro---ProHisValLeu	215
226	ACCCAAAAATAGCCTACCATGCTCGCTCGGGCTGCGCTTACCTGCACCAAGAA-----	279
216	Val---AsnTrpAlaValGlnIleAlaArgGlyMetHisTyRLeuHisCysGluAlaLeu	234
280	---AACATCATCTCTGTACCTGAAGTCGGACAAATCTGTGTGTGG-----TTC	327
235	ValProValIleHisArgAspLeuLysSerAsnAsnIleLeuLeuLeuGlnProIleGlu	254
328	CTTGACGTCAAGCAGACATCAACATCAAGCTATCTGACTACGGGATTTCCGAGCGAGTCA	387
255	SerAspAspMetGluHisLysThrLeuLysIleThrAspPheGlyLeuAlaArgGluTrp	274
388	TTCCATGAGGGCGCCCTTAGCGGTGGAGGGCACTCTCTGGCTACACGGCCCGCAGAGATCAGG	447
275	HisLysThrThrGlnMetSerAlaAlaGlyThrTyRAlaTrpMetAlaProGluValIle	294
448	CCTCGCATTTATATGATGAGGAAGTAGATGTTCTCTTCATGGAAATGGTGCTCTACGAG	507
295	LysAlaSerThrPheSerLysGlySerAspValTrpSerPheGlyValLeuLeuTrpGlu	314
508	TTCTCTCAGCAGCAGCGCCCTGCATCTGGGGCCACACACAGTCCAGATTGGC-----	558
315	LeuLeuThrGlyGlnValProTyRArgGlyIleAspCysLeuAlaAlaIleTyRVal	334
559	-----AAGAAGCTGTCCAAGGGCATCCGCCGCTTCGGGGCAGCGGAGGAAGTCAG	612
335	AlaValAsnLysLeuThrLeuProIleProSerThrCysProGluPro-----	350
613	TTCCGGGAGCTCAGGGCGCTCATGTATGGATGCTGGGACACTAAGCCAGGAGACGACCG	672
351	-----PheAlaGlnLeuMetAlaAspCysTrpAlaGlnAspProHisArgArg---	366
673	CTGGCCCTGTCTGGTGTAGCCAGATGAAGGAGCCCGACTTTTGGCCACTTTCATGTATGAA	732

367 -----ProAspPheAlaSerIleLeuGln 375

733 CTGTG-CTGTGGGAGACAGACCCCTTCTCTCATCCAGGCCAGGAGTACACCGTGT 791

376 LeuGlnAlaLeuGlnAlaGlnValLeuArgGluMetProCArgAspSerPheHisSerMet 395

792 GTTTTGGGATGGAAAAGAGAGTCCAG- 818

396 GlnGluGlyTrpLysArgGluIleGlnGlyLeuPheAspGluLeuArgAlaLysGluLys 415

818 ----- 818

416 GluLeuLeuSerArgGluGluGluThrArgAlaAlaArgGluGlnArgSerGlnAla 435

819 ---GAATCACGGTGTGTGAACAC- 839

436 GluGlnLeuArgArgGluHisLeuLeuAlaGlnTrpGluLeuGluValPheGluArg 455

840 -----AGAGAAGGCCCTCAT- 855

456 GluLeuThrLeuLeuGlnGlnValAspArgGluArgProHisValArgArgArgArg 475

855 -----GGAGTGCAGAGGATGCTGCGCC 878

476 GlyThrPheLysArgSerLysLeuArgAlaArgAspGlyGlyuArgIleSerMetPro 495

879 TGGGATGAAGGTGAGCTG- 896

496 LeuAspPheLysHisArgIleThrValGlnAlaSerProGlyLeuAspArgArgArgAsn 515

897 -----CCAGTCCAGGTCGAGATGCCCTGT- 922

516 ValPheGluValGlyProGlyAspSerProThrPheProCArgPheArgAlaIleGlnLeu 535

923 -----GGACAG- 949

536 GluProAlaGluProGlyGlnAlaTrpGlyArgGlnSerProArgArgLeuGluAspSer 555

950 ACATCTACACCTCAAGGCGATGTGCCCTTAAACACACCCCAACAGGCCCTTGATATCT 1009

556 SerAsnGlyGluArgAlaCys- 566

1010 CAGCTGTCGTACCTGCTCTTGGCGCTGCTTATTAATAAGA- 1054

567 GlyProSerSerProLysProGlyGluAlaGlnAsnGlyArgArgSerArgMetAsp 586

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587 GluAlaThrTrpLysLeuAspSerAspAspSerProLeuGlySerProSerThrPro 606

1106 CCGTGGTGC---GGGCGACCCCAAGGACAGTGTCTCTACTGTGCTTCACACAGCCA 1162

607 ProAlaLeuAsnGlyAsnProArg- 623

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624 LysArgProValProAlaGluArgGlySerSerGly---ThrPro- 638

1223 CCATGGAGGTGGTCAACAGCGGCTCTGAGTCTGTGTACAGCAATGGCGGCGCTCTTG 1282

639 -----LysLeuIleGlnArgAlaLeuLeuArgGlyThrAlaLeu---LeuAlaSerLeu 655

1283 -----TCATCG 1288

656 GlyLeuGlyArgAspLeuGlnProProGlyGlyProGlyArgGluArgGlyGluSerPro 675

1289 ACTGTGCTCCCTGGAGATCTGAGCGGCTGGAGCCCTTACATGGCCCGCTCCATGGTTA 1348

676 ThrThrProProThrProThrProAlaPro---CysProThrGluProProPro- 693

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694 ProLeuIleCysPheSerLysThrProAspSerProProThrProAlaProLeuLeu 713

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1479 |||:|||||:
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1538 -----GCCACAGCGCCACCAAGGTGCTGTAGGGGACTCCATCGCGAGC 1585
1539 |||:|||||:
760 ProLeuGlyLeuIleSerArgPro-----ArgProSerProLeuArgSer 774
1586 TGAGCATCATGTACAGTAGAGAGCTGGGCGACGACATCTGATCCACCAAGATCACTCA 1645
1587 |||:|||||:
775 -----ArgIleAspProTrp-----Ser 780
1646 CTGACTACTGCTCCATGCTCTCTACTCTCATCCACCCGCGCAGGCTGCCAGGTCCC 1705
1647 |||:|||||:
781 PheValSerAla-----GlyProArgProSerProLeuProSerPro 794
1706 CTTCAAGCTCTCCAGCTCCCGAGCAAGTTCTTCCAGTGTCCCTTCTCCACGAGTGG 1765
1707 |||:|||||:
795 -----GlnProAlaProArgAla---ProTrpThrLeuPheProAspSerAsp 810
1766 AGGACTCAGACATGTACATACGCCCGGTGCTGCTCGCAGAGTCTTGAGCATGACCTGA 1825
810 ----- 810
1826 CCCCCATGAGCGGGAGACCT---TCAGCCAGACCTGCAGCGCGTGAAGATCTCGCG 1882
811 ProPheTrpAspSerProProAlaasn-ProPheGlnGlyProGlnAspCysArgAl 830
1883 TCAGACACTCATTTGGTCCCGACAGCGCGGTGG 1916
830 aGlnThrLysAspMetGlyAlaGlnAlaProTrp 841
JLT 8
10-115-482-48
sequence 48, Application US/10115482
Application No. US20030212257A1
GENERAL INFORMATION:
APPLICANT: Spytek, et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: AND METHODS
TITLE OF INVENTION: OF USING THE SAME
FILE REFERENCE: 21404-322D
CURRENT APPLICATION NUMBER: US/10/115,482
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: 60/285,890
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 60/286,068
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/286,292
PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/287,213
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/288,257
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/291,134
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/291,725
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/294,771
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/296,965
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/299,128
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 48
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-115-482-48
Alignment Scores:
Pred. No.: 7,49e-13 Length: 915
Score: 335.50 Matches: 106
Percent Similarity: 46.19% Conservative: 76
Best Local Similarity: 26.90% Mismatches: 159
Query Match: 8.27% Indels: 53
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DB 318 LeuCysHisLeuHisHisProSerLeuIleSerLeuAlaAlaGlyIleArgProArg 337
QY 130 TGCTTGGCGCTGGAGCTCGCGCGCTCAGGAGCTCAACACCGCTGTGTCGAGAACGCC 189
DB 338 MetLeuValMetGluLeuAlaSerLysGlySerLeuAspArgLeuGlnGlnAspLys 357
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DB 358 AlaSer-----LeuThrArgThrLeuGlnHisArgIleAlaLeuHisVal 372
QY 250 GCTCGGCGCTGGCGCTACCTGCACAGAAACATCATCTTCTGTGACCTGAAGTCGGAC 309
DB 373 AlaAspGlyLeuArgTyLeuHisSerAlaMetIleIleTyArgAspLeuLysProHis 392
QY 310 AACATTCGTGTGTGCTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTAC 369
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QY 370 GGGATTTCAGCGAGTCAATTCATGACGGGCGCCCTAGCGGTGGAGGCGCATCTCTGGTAC 429
DB 413 GlyIleAlaGlnTyCysCysArgMetGlyIleLysThrSerGluGlyThrProGlyPhe 432
QY 430 CAGGCGCCCGAGATC---AGGCTCGCATTTATATGATGAGAGGTAGATATGTTCTTCC 486
DB 433 ArgAlaProGluValAlaArgGlyAsnValIleTyArgGlnGlnAlaAspValTySer 452
QY 487 TATGAATGGTCTCTACGAGTGTCTG---TCAGACAGCGCCCTGCATCGGGC----- 537
DB 453 PheGlyLeuLeuLeuTyArgAspIleLeuThrThrGlyGlyArgIleValGluGlyLeuLys 472
QY 538 -----CACCACAGCTCCAGATTGCCAAGAGCTGTCCAAGGGCATCCGCCCG 585
DB 473 PheProAsnGlnPheAspGluLeuGlnGlyLysLeuProAspProValLysGlu 492
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586 GTTCTGGGGCAGCCGAGAGAGTGCAGTTCCTCGGAGACTGCAGGGCTCATGTGGAGTGC 645  
493 TyrGlyCysAlaPro-----TTPProMetValGluLysLeuLeuLysGlnCys 508  
646 TGGGACACTAAGCAGAGAGCCGCTGCGCTGCGTGGTGGAGCCAGATGAAGGAC 705  
509 LeuLysGluAsnProGlnGluArgProThrSerAlaGlnValPheSerGlnValPheAsp 528  
706 CCGACTTTTGGCACTTCATGATGAATGCTGCTGGGAGACGAG----- 750  
529 IleLeuAsnSerAla-----GluLeuValCysLeuThrArgAlaGlnLeuLeuPro 545  
751 -----ACAGCCTTCTCTCATCCAGGGCCAGGAGTACACCGTGGTGT 795  
546 LysAsnValIleValGluCysMetValAlaThrHisAsnSerArgAsnAlaSerIle 565  
796 TGGGATGGA-----AAAGAGAGTCCAGGAACTACACGGTGGTGAACACAGAG 843  
566 TrpLeuGlyCysGlyHisThrAspArgGlyGlnLeuSerPheLeuAspLeuAsnThrGlu 585  
844 AAGGCGCTCAGGAGTG-----CAGAGGATGTGCTGCCCTGGGATGAAGGTGAGC 894  
586 GlyTyrThrSerGluValAlaAspSerArgIleLeuCysLeuAlaLeu----- 602  
895 TCCAGCTCCAGTCCAGTCCAGTCCCTGTGG-----ACAGCCAGCCAGGACCAGAAATC 948  
603 ValHisLeuProValGluLysGlnSerTrpIleValSerGlyThrGlnSerGlyThrLeu 922  
949 TACATCTACACCTCAAGGGATGTGCCCCCTTAACACACCCCAAGGCTTGGATACT 1008  
623 LeuValIleAsnThrGluAspGlyLysArgHisThrLeuGluLysMetThrAspSer 642  
1009 CCAGCTGCTGCTACCTGCTTCTTGGCCGCTGCTGTATTAA-----AAGATTCCTAC 1062  
643 -----ValThrCysLeuTyrCysAsnSerPheSerLysGlnSerLysGlnLysAsn 659  
1063 CTGGCTTTAGCGGGCTCCCGCATGGGCTTGTGCTGTGTTT 1104  
660 PheLeuLeuValGlyThrAlaAspGlyLysLeuAlaIlePhe 673

LT 9  
0-115-482-50  
quence 50, Application US/10115482  
blication NO. US20030212257A1  
NERAL INFORMATION:  
PLICANT: Sovtek, et al.  
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM  
TITLE OF INVENTION: AND METHODS  
TITLE OF INVENTION: OF USING THE SAME  
FILE REFERENCE: 21404-322D  
CURRENT APPLICATION NUMBER: US/10/115,482  
URRNT FILING DATE: 2002-04-05  
ROR FILING DATE: 2002-04-05  
ROR FILING DATE: 2001-04-05  
ROR FILING DATE: 2001-04-03  
ROR APPLICATION NUMBER: 60/281,136  
ROR FILING DATE: 2001-04-03  
ROR APPLICATION NUMBER: 60/281,863  
ROR FILING DATE: 2001-04-05  
ROR APPLICATION NUMBER: 60/281,906  
ROR FILING DATE: 2001-04-05  
ROR APPLICATION NUMBER: 60/282,934  
ROR FILING DATE: 2001-04-10  
ROR APPLICATION NUMBER: 60/283,512  
ROR FILING DATE: 2001-04-12  
ROR APPLICATION NUMBER: 60/285,325  
ROR FILING DATE: 2001-04-19  
ROR APPLICATION NUMBER: 60/285,890  
ROR FILING DATE: 2001-04-23  
ROR APPLICATION NUMBER: 60/286,068  
ROR FILING DATE: 2001-04-24  
ROR APPLICATION NUMBER: 60/286,292  
ROR FILING DATE: 2001-04-25  
ROR APPLICATION NUMBER: 60/287,213

/ PRIOR FILING DATE: 2001-04-27  
/ PRIOR APPLICATION NUMBER: 60/288,257  
/ PRIOR FILING DATE: 2001-05-02  
/ PRIOR APPLICATION NUMBER: 60/291,134  
/ PRIOR FILING DATE: 2001-05-15  
/ PRIOR APPLICATION NUMBER: 60/282,020  
/ PRIOR FILING DATE: 2001-04-06  
/ PRIOR APPLICATION NUMBER: 60/291,725  
/ PRIOR FILING DATE: 2001-05-17  
/ PRIOR APPLICATION NUMBER: 60/294,771  
/ PRIOR FILING DATE: 2001-05-31  
/ PRIOR APPLICATION NUMBER: 60/296,965  
/ PRIOR FILING DATE: 2001-06-08  
/ PRIOR APPLICATION NUMBER: 60/299,128  
/ PRIOR FILING DATE: 2001-06-08  
/ NUMBER OF SEQ ID NOS: 149  
/ SEQ ID NO 50  
/ LENGTH: 911  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ US-10-115-482-50

Alignment Scores:  
Pred. No.: 2,36e-12 Length: 911  
Score: 327.50 Matches: 101  
Percent Similarity: 45.48% Conservative: 75  
Best Local Similarity: 26.10% Mismatches: 168  
Query Match: 8.0% Indels: 43  
DB: 12 Gaps: 13

US-09-836-392-8\_COPY\_22\_2205 (1-2184) x US-10-115-482-50 (1-911)

QY 28 GCCATGAAGAACTTCTCCGAG-----TTCGGCAGAGGCCAGCATG 69  
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QY 70 CTGACCGCTGAGCAGCCCTCATCGTGGCGCTCATCGGCATCAGCATCCACCCTC 129  
DB 318 LeuCysHisLeuHisHisProSerLeuLeuLeuLeuAlaGlyIleArgProArg 337  
QY 130 TGCTTCGCTGAGGCTCGCGCTCAGCAGCCTCAACACCGTGTCTCCGAGACGCC 189  
DB 338 MetLeuValMetGluLeuAlaSerLysGlySerLeuAspArgLeuGlnAspLys 357  
QY 190 AGATTCTTCTTTATATACCCCTGGGACACATCTCCACCAAAAATAGCTACCATC 249  
DB 358 AlaSer-----LeuThrArgThrLeuGlnHisArgIleAlaLeuHisVal 372  
QY 250 GCCTCGGCTGGCTTACCTGACACAGAAAAACATCATCTTCTGTGACCTGAGTGGAC 309  
DB 373 AlaAspGlyLeuArgTyrLeuHisSerAlaMetIleIleTyrArgAspLeuLysProHis 392  
QY 310 AACATTCTGTGTGCTCCCTTGAGTCAAGGACCATCAACATCAAGCTATCTGACTAC 369  
DB 393 AsnValLeuLeuPheThrLeuTyrProAsnAlaAlaIleAlaLysIleAlaAspTyr 412  
QY 370 GGGATTTCGAGCAGTCAATTCATGAGGGCGCCCTAGGCGTGGAGGGGCACTCTGCTAC 429  
DB 413 GlyIleAlaGlnTyrCysCysArgMetGlyIleLysThrSerGluGlyThrProGlyPhe 432  
QY 430 CAGGCCCCAGAGATC---AGGCTCGCATTTGATATATGAGAGAGGTAGATATGTTCTCC 486  
DB 433 ArgAlaProGluValAlaArgGlyAsnValIleTyrAsnGlnGlnAlaAspValTyrSer 452  
QY 487 TATCGAATGTGCTCTACGAGTTGCTG---TCAGGACAGCGCCCTGCATCTGGGC----- 537  
DB 453 PheGlyLeuLeuLeuTyrAspIleLeuThrThrGlyArgIleValGluGlyLeuLys 472  
QY 538 -----CACCACAGCTCCAGATTGCCAAGAGGTGCCAAGGGGCATCCGCCCG 585  
DB 473 PheProAsnGluPheAspGluLeuGluIleGlnGlyLysLeuProAspProValLysGlu 492  
QY 586 GTTCTGGGCGCAGCGGAGAGAGTGCATTTCCGGCGAGTTCAGCGCGCTCATGTGGAGTGC 645

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646 TGGGACACTAAGCCAGAGAGCGCGCTGCGCTGCTGGTGGTGGAGCCAGATGAAGGAC 705 70 CTGCACCGCTGCAGCAGCAGCCCTGCATCGTGGCGCTCATCGCATCAGCATCCACCGCTC 129  
509 LeuLysGluAsnProGlnGluArgProThrSerAlaGlnValPheAspIleLeuAsnSer 528 1221 LeuCysHisLeuHisHisProSerLeuIleSerLeuLeuAlaAlaGlyIleArgProArg 1240  
706 CCGACTTTTCCACCTTCATGATGAAGTGTGTGGGAGCAGACACA-:::GCC 1241 MetLeuValMetGluLeuAlaSerLysGlySerLeuAspArgLeuLeuGlnGlnAspLys 1260  
529 AlaGluLeuValCysLeuThrArgArgIleLeuLeuProLysAsnValIleValGluCys 548 190 AGAATTCCTTCCTTTATACCCCTGGGACACATCTCACCACCAAAATAGCCTACCATC 249  
757 TTCTTCTCATCCAGGCGCAGAGTACACCGTGGTGTGGGATGGA-::: 1261 AlaSer-:::LeuThrArgThrLeuGlnHisArgIleAlaLeuHisVal 1275  
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805 AAAGAGGAGTCCAGGAACTACACGGTGTGTGAACACAGAGAGGCGCTCATCGAGGTG- 861 1276 AlaAspGlyLeuArgGlyLeuHisSerAlaMetIleIleThrArgAspLeuLysProHis 1295  
569 AspArgGlyGlnLeuSerPheLeuAspLeuAsnThrGluGlyThrSerGluGluVal 588 310 AACATTCCTGGTGTGGTCCCTTGACCTCAAGGAGCAGATCAACATCAAGCTATCTGACTAC 369  
862 -----CAGAGATGTGCTGCTGGGATGAGGTGAGCTCCAGCTCCAGTCCAGAGA 915 1296 AsnValLeuLeuPheThrLeuTyrProAsnAlaAlaIleIleAlaLysIleAlaAspTyr 1315  
589 AlaAspSerArgIleLeuCysLeuAlaLeu-:::ValHisLeuProValGluLys 605 370 GGGATTCGAGGAGTCAATCCATGAGGCGCGCTAGCGGTGAGGGGACCTCTCGCTAC 429  
916 TCCTGTGG-:::ACAGCCAGGAGCAGACCAAAATCTACATCTACACCTCAAGGCGC 969 1316 GlyIleAlaGlnTyrCysCysArgMetGlyIleLysThrSerGluGlyThrProGlyPhe 1335  
606 GluSerTrpIleValSerGlyThrGlnSerGlyThrLeuLeuValIleAsnThrGluAsp 625 430 CAGGCGCCAGAGATC-:::AGGCTCGCATTTGTATATGATGAGAGAGGTAGATATGTCTCC 486  
970 ATGTGCGCTTAAACACCCCAACAGGCGCTTGGATATCCAGCTGTGCTACCTGCTTC 1029 1336 ArgAlaProGluValAlaArgGlyAsnValIleThrAsnGlnGlnAlaAspValTyrSer 1355  
626 GlyLysArgHisThrLeuGluLysMetThrAspSer-:::ValThrCysLeu 642 487 TATGGAATGTGCTCTACGAGTTGCTG-:::TCAGGACAGCGCGCTGCTGAGGCGC 537  
1030 TTGGCGGTGCTGTATTAA-:::AAGATTCCTACCTGCTTGTAGGCGGCTCGCC 1083 1356 PheGlyLeuLeuTyrAspIleLeuThrThrGlyArgIleValGluGlyLeuLys 1375  
643 TyrCysAsnSerPheSerLysGlnSerLysAsnPheLeuLeuValGlyThrAla 662 538 -----CACCACGAGTCCAGATTCGCAAGAGAGCTGTCGAAGGCGCATCCGCGCGC 585  
1084 GATGCGCTGTGCTGTGTT 1104 1376 PheProAsnGluPheAspGluLeuGluIleGlyLysLeuProAspProValLysGlu 1395  
663 AspGlyLysLeuAlaIlePhe 669 586 GTTCTGGGCGCAGCGGAGAGTGCAGTTCGCGGCTGCGCTGCTGAGCGGCTCATGTGAGTGC 645  
110-335-687A-2 1396 TyrGlyCysAlaPro-:::TipProMetValGluLysLeuIleLysGlnCys 1411  
646 TGGGACACTAAGCCAGAGAGCGCGCTGCGCTGCTGAGCGGCTGAGTGAAGGAC 705 1412 LeuLysGluAsnProGlnGluArgProThrSerAlaGlnValPheAspIleLeuAsnSer 1431  
706 CCGACTTTTCCACCTTCATGATGAAGTGTGTGGGAGCAGACA-:::GCC 756 1432 AlaGluLeuValCysLeuThrArgArgIleLeuLeuProLysAsnValIleValGluCys 1451  
757 TTCTTCTCATCCAGGCGCAGAGTACACCGTGTGTGGGATGGA-::: 804 1452 MetValAlaThrHisHisAsnSerArgAsnAlaSerIleThrLeuGlyCysGlyHisThr 1471  
805 AAAGAGGAGTCCAGGAACTACACGGTGTGTGAACACAGAGAGGCGCTCATGGAGGTG- 861 1472 AspArgGlyGlnLeuSerPheLeuAspLeuAsnThrGluGlyThrSerGluGluVal 1491  
862 -----CAGAGATGTGCTGCTGGGATGAGGTGAGCTGCCAGTCCAGTCCAGAGA 915 1492 AlaAspSerArgIleLeuCysLeuAlaLeu-:::ValHisLeuProValGluLys 1508  
1492 AlaAspSerArgIleLeuCysLeuAlaLeu-:::ValHisLeuProValGluLys 1508 916 TCCTGTGG-:::ACAGCCAGGAGGAGCAGAAAAATCTACATCTACACCTCAAGGCGC 969  
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1529 GlyLysLysArgHisThrLeuGluLysMetThrAspSer-:::ValThrCysLeu 1545 1030 TTGGCGGTGCTGTATTAA-:::AAGATTCCTACCTGCTTGTAGGCGGCTCGCC 1083  
1546 TyrCysAsnSerPheSerLysGlnSerLysAsnPheLeuLeuValGlyThrAla 1565 28 GCCATGAAGAACTTCTCCAG-:::TTCCGCGCAGGAGCGCAGCATG 69  
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ment Scores:  
a. No.: 2.6e-12  
re: 327.50  
cent Similarity: 45.48%  
t Local Similarity: 26.10%  
ry Match: 12

ILT 10

10-335-687A-2

Sequence 2, Application US/10335687A

Publication No. US20030166222A1

GENERAL INFORMATION:

APPLICANT: Meyers, Rachel E.

APPLICANT: Millennium Pharmaceuticals, Inc.

TITLE OF INVENTION: 39267, Human Kinase Family Members and

FILE REFERENCE: MPI02-001PIRM

CURRENT APPLICATION NUMBER: US/10/335,687A

CURRENT FILING DATE: 2003-01-02

PRIOR APPLICATION NUMBER: 60/345,773

PRIOR FILING DATE: 2002-01-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1818

TYPE: PRT

ORGANISM: Homo sapiens

10-335-687A-2

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JLT 11
10-335-687A-5
sequence 5, Application US/10335687A
Application No. US20030166222A1
GENERAL INFORMATION:
APPLICANT: Millenium Pharmaceuticals, Inc.
TITLE OF INVENTION: 39267, Human Kinase Family Members and
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: MP102-001PRNM
CURRENT APPLICATION NUMBER: US/10/335,687A
CURRENT FILING DATE: 2003-01-02
PRIORITY APPLICATION NUMBER: 60/345,773
PRIORITY FILING DATE: 2002-01-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1824
TYPE: PRT
ORGANISM: Homo sapiens
10-335-687A-5

Alignment Scores:
L. No.: 2,6e-12 Length: 1824
Percent Similarity: 45.48% Matches: 101
Local Similarity: 26.10% Conservative: 75
Indels: 43 Mismatches: 168
Gaps: 12

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70 CTGACGGCTGAGACCCCTGATCTGCGGCTCATCGGCATCAGCATCCACCGCTC 129
||||| :|||:|||||
1221 LeuCysHisLeuHisProSerLeuLeuLeuAlaAlaGlyIleArgProArg 1240
130 TGCTTCGCTGAGCTGCGCGCTCAGCAGCCTCAACACCGTGTCTCCGAGACGCC 189
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1241 MetLeuValMetGluLeuAlaSerLysGlySerLeuAspArgLeuLeuGlnAspLys 1260
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1261 AlaSer-----LeuThrArgThrLeuGlnHisArgIleAlaLeuHisVal 1275
250 GCTCGGGCTGCTTACCTGACACAGAAACATCATCTTCTGTGACCTGAGTCGGAC 309
||||| :|||:|||||
1276 AlaAspGlyLeuArgTyLeuHisSerAlaMetIleIleTyArgAspLeuLysProHis 1295
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487 TATGGAATGCTCTACAGGTGCTG---TCAGACAGCCCTTCGACTCGGCG--- 537
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1356 PheGlyLeuLeuLeuTyAspIleLeuThrThrGlyGlyArgIleValGluGlyLeuLys 1375

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Db	362	AlaValAsnLysLeuAlaLeuProLeProSerThrCysProGluPro-----	377
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QY	673	CTGGCCCTGTCGGTGTGTGACCGAGATGAAGACCCGACTTTTGGCCACTTCATG	732
Db	394	-----ProSerPheThrAsnLeuLeuLeuAspGln	402
QY	733	CTGTGCTGTGGGAAGACAGACAGCCTTCTTCTC-ATCCAGAGCGCCAGAGTACAC	791
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QY	792	CTTTTGGGATGGAAAACAGAGTCCAGGAACCTACACGGT-----GGTGAACACAG	842
Db	423	GlnAspAsnTrpHisIleGluIleGlnGluMetPheAspGlnLeuArgAlaLysGlu	442
QY	843	GAA-----GGGCTCATGGAGGTGCAGAG	866
Db	443	GluLeuArgThrTrpGluGluLeuThrArgAlaLeuGlnGlnLysAsnGlnGlu	462
QY	867	GATGTGTCCTCGGATGAAGTGAAGTGCAGGTCCAGTCCAGTCCAGAGAT-----	916
Db	463	GluLeuLeuArgArgGluGluGlnLeu-Leu-AlaGluArgGluIleAspIleLeuGlu	482
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QY	947	-----TCTACATCTACACCT	962
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QY	963	CAAGG-----GCATGTGCCCTTAAACACACCCCAACAGGCCTT	1001
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QY	1074	GGGCT-----	1079
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Db	641	ProAlaLeuProGlyPheThrSerLeuMetGluMet-----	652
QY	1194	CGCAGCGAGAACCCCTACCCAGTGAAGCCATGAGGTGTCAACAGCGCTCTGAGGT	1253
Db	653	-----GluAspGluAspSerGluGlyProGlySerGlyGluSerArgLeu-----	667
QY	1254	CTGTGTACAGCAATGGGCGCGCTCTCTGTATCATGCTGTGCTCCCT-----	1301
Db	668	-----GlnHisSerProSerGlnSerTyrlLeuCysIleProPheProArgGly	683
QY	1302	-----GGAGATCTGCAGCGCGGTGGAGCCCTACAT-----GGCCCCCTCCATG	1346

684 GluAspGlyAspGlyProSerSerAspGlyLeHisGluGluProThrProValAsnSer 703  
1347 TACGTCAGTCGTCGACGCTCGAGG-----CAGAGGGAGGAGGTCGTCG 1394  
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722 -----HisHis-----ArgArg 725  
1455 TGCCCGGTACTTCTCGGGGT-----CCACAGCCGCCCT----- 1475  
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1476 -----CCACAGCCGCCCT----- 1487  
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1575 CATCGCGAGTGAGCATCATGTACAGTGAGGAGTGCGGCACGAGATCCTGATCCACCA 1634  
805 oSerAlaSerLeuThrLeuLeu----- 812  
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813 -----SerLeuSerSerIleSerGluCysAsnSerThrArgSe 825  
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845 uAla-----ProLeuSerProCysThrHisAsnProLeuValAsnValArgVa 862  
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882 rProSerGlnProSerSerHisArgArgThrProSerAspGlyAlaLeuLysProGluTh 902  
1857 CTGACGCGCGTGAAGATCCTCGCCCTCAGACACCTCATTTGGGTCCCGAGCGCGGTGG 1916  
902 rLeuLeuAlaSer-ArgSerProSerSerAsnGlyLeuSerProSerProGlyAlaGlyG 922  
1917 AGATGTTATCGTCAATTGGCTGGAGAGATTCCTGAAGCCAGCGGGGCGAGTCATGTC 1976  
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1977 CGTCT 1981  
942 rOSeR 943

LT 13  
0-153-668-438  
quence 438, Application US/10153668  
lication No. US20030092616A1  
ENRAL INFORMATION:  
APPLICANT: HONDA, Goichi  
APPLICANT: MATSUDA, Akio  
APPLICANT: MURAMATSU, Shuji  
APPLICANT: ISHIZAWA, Kenya  
TITLE OF INVENTION: STATE Activating Gene  
FILE REFERENCE: 1254-0207P

LT 13

0-153-668-438

Sequence 438. Application US/10153668

Sequence 436, Application US/10-  
Application No. US20030092616A1

GENERAL INFORMATION:

APPLICANT: HONDA, Goichi

APPLICANT: MATSUDA, AKIO

APPLICANT: MURAMATSU, Shuji

APPLICANT: ISHIZAWA, Kenya

TITLE OF INVENTION: STAT6 Activating Gene

FILE REFERENCE: 1254-0207P

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, , CURRENT APPLICATION NUMBER: US/10/153,568
, , CURRENT FILING DATE: 2002-05-24
, , PRIOR APPLICATION NUMBER: US 60/293,172
, , PRIOR FILING DATE: 2001-05-25
, , PRIOR APPLICATION NUMBER: US 60/316,031
, , PRIOR FILING DATE: 2001-08-31
, , PRIOR APPLICATION NUMBER: US 60/328,403
, , PRIOR FILING DATE: 2001-10-12
, , PRIOR APPLICATION NUMBER: JP 2001-157043
, , PRIOR FILING DATE: 2001-05-25
, , PRIOR APPLICATION NUMBER: JP 2001-260691
, , PRIOR FILING DATE: 2001-08-30
, , PRIOR APPLICATION NUMBER: JP 2001-313175
, , PRIOR FILING DATE: 2001-10-10
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US-10-153-568-438

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Best Local Similarity:	22.4%	Mismatches:
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US-09-836-392-8 COPY 22 2205 (1-2184) X US-10-153-668-438 (1-892)

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Db	223	MetGluPheCysAlaGlnGlyGlnLeuTyrGluValLeuArgAlaGlyArg	239
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Db	240	-----ProValThrProSerLeuValAspTrpSerMetGlyIleAlaGlyGly	256
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QY	319	GTGTGGTCCCTTGACGTCAAGGACACATCAACATCAAGCTATTCTGACTACGGGATTTCG	378
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QY	496	GTGCTCTACGAGTTGCTGTCCAGACAGCGCCCT-----	528
Db	332	ValLeuTrpGluLeuLeuThrGlyGluIleProTyrLysAspValAspSerSerAlaIle	351
QY	529	-----GCATGGCGCCACCACCGCTCCAGATTGCCAAGAAGCTGCCAAGGGCATCCGC	582
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QY	583	CCGCTTCTGGGCGCAGCCGAGGAAGTGCAGTTCCGGCGACTCCAGCGCTCATGATGGAG	642

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379 CysTrpAsnSerLysProArgAsnArgProSerPheArgGlnIleLeuLeuHisLeuAsp 398
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685 GTGTGTAGCCAGATGAAGGACCGCACTTTTGCCACCTTCATGTATGAACATGCTGCTGGG 744
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399 IleAlaSerAla-----AspValLeuSerThr 407
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745 AAGCAGACACCTTCTCTCATCCAGGCCAG-----GAGTAC 783
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408 ProGlnGluThrTyrPheLysSerGlnAlaGluTrpArgGluValLysLeuHisPhe 427
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
784 ACCGTGTGTTTTGGATGGA----- 804
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
428 GluLysIleLysSerGluGlyThrCysLeuHisAsgLeuGluGluLeuValMetArg 447
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
505 ---AAAGAGAGATCCAGAAC----- 822
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
448 ArgArgGluGluLeuArgHisAlaLeuAspIleAsgGluHisTyrGluAsgLysLeuGlu 467
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823 -----TACACGGTGGTGAACACA-----GAG 843
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468 ArgAlaAsnAsnLeuTyrMetGluLeuAsnAlaLeuMetLeuGlnLeuGluLeuLysGlu 487
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    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
488 ArgGluLeuLeuArgArgGluGlnAlaLeuGluAsgAsgCysProGlyLeuLeuLys-Pr 507
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895 TGCCAGCTCCAGGTCCAGAGATCCCTGTGCAGCACCGCAGGACCGAGAAATCTACATC 954
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
507 ChiProSerArgGlyLeuLeuHisGlyAsnThrMetGluLysLeuLeuLysLysArgAs 527
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
955 TACACCTCAAGGCGATGTGCCCTTTAAACACACACCCCAAGCGCTGGATPACTCCAGCT 1014
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
527 nValProGlnLysLeuSer-----ProHisSerLysArgProAspIleLeuLysAl 544
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544 aGluSer-----LeuLeuProLysLeuLeuAspAlaAl 554
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554 aLeuSerGlyValGlyLeu----- 560
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561 ---ProGlyCysProLysAlaProProSer---ProGlyArgSerArgGlyLysThr 578
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
1195 GCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTCAGGTC 1254
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
578 rArgHisArg-----LysAlaSerAlaLys 586
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
1255 TGGTACAGCAATGGCGCGGCGCTCTTGTCAATCGACTGTGCTCCCTGGAGATCTGCAGG 1314
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
586 sGlySerCysGlyAspLeuProGlyLeuArgThrAlaValProProHisGluProGlyGly 606
    |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
1315 CGGTGGAGCCCT-----ACATCGGCC-----CTCCCATG 1344
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1345 GTTACGT-----CA 1353
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626 aLeuArgGlyLeuHisAspLeuLeuLeuArgLysMetSerSerSerSerProAspLe 646
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1354 CTCGTGTGCACCTCTGAGGCGACAGGGGAGGAGTGTCTGTGTGCTG-----ATGAC 1407
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646 uLeuSerAlaAlaLeuGlySerArgGlyArgGlyAlaThrGlyGlyAlaGlyAspProGly 666
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Qy	1527	-----CCCGCGACGCCACACAGGCC-----	1548
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Db	741	AlaValThrArgSerGlnLysArgGlyIleSerSerGluGluGluGlyValasp	760
Qy	1579	GGGACAGTGACATCATGTACAGTAGGAGCTGGCAGCGCAGATCCTCATCCACACGAA	1638
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Qy	1639	TCATCACTGACTACTGCTCTCATGTCCTCTACTCTCTATCCCAACCCCGCCAGGCTGCC	1698
Db	780	-----SerLeuSerThrPheSerSerGluAsnProSerAspGlyGlu	793
Qy	1699	AGGTCCCTCAAGCCTCCACAGTCTCCAGCAAGTCTTCCAGTGTCCTTTCTCCACC	1758
Db	794	GluGlyThrAlaSerGluPro---SerProSerGlyThrProGluValGly---SerThr	811
Qy	1759	GACTCGAGGACTCAGACATGCTACTACATACGCGCGTGTCTCGACAGTCTGAGCAT	1818
Db	812	AsnThrAspGluArgProAspGluArgSerAspMetCysSerGlnGlySerGluIle	831
Qy	1819	GACCTGACCCCATGACGGGGAG	1842
Db	832	ProLeuAspProProProSerGlu	839
RESULT 14			
US-10-153-668-324			
; Sequence 324, Application US/10153668			
; Publication No. US2003092616A1			
; GENERAL INFORMATION:			
; APPLICANT: HONDA, Goichi			
; APPLICANT: MATSUDA, Akio			
; APPLICANT: MURAMATSU, Shuji			
; APPLICANT: ISHIZAWA, Kenya			
; TITLE OF INVENTION: STAT6 Activating Gene			
; FILE REFERENCE: 1254-0207P			
; CURRENT APPLICATION NUMBER: US/10/153,668			
; CURRENT FILING DATE: 2002-05-24			
; PRIORITY APPLICATION NUMBER: US 60/293,172			
; PRIORITY FILING DATE: 2001-05-25			
; PRIORITY APPLICATION NUMBER: US 60/316,031			
; PRIORITY FILING DATE: 2001-08-31			
; PRIORITY APPLICATION NUMBER: US 60/328,403			
; PRIORITY FILING DATE: 2001-10-12			
; PRIORITY APPLICATION NUMBER: JP 2001-157043			
; PRIORITY FILING DATE: 2001-05-25			
; PRIORITY APPLICATION NUMBER: JP 2001-260681			
; PRIORITY FILING DATE: 2001-08-30			
; PRIORITY APPLICATION NUMBER: JP 2001-313175			
; PRIORITY FILING DATE: 2001-10-10			
; NUMBER OF SEQ ID NOS: 488			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 324			
; LENGTH: 859			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-153-668-324			
Alignment Scores:		2.33e-10	859
Ref. No.:			

Alignment Scores: 2.33e-10 Length: 859  
Pred. NO.:

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t Local Similarity: 34.27%   Conservative: 89
ry Match: 22.40%    Mismatches: 257
              7.28%   Indels: 236
              15      Gaps: 31

09-836-392-8_COPY_22_2205 (1-2184) x US-10-153-668-324 (1-959)

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85  CACCCTGTGATGTGGCGCTCATCGGATCAGCATCCACCCTGTGTTCCGCC-----138
   |||::|||
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139  CTGGAGTCCGCGCCCTCAGCAGCTCAACACCGTCTGTCGGAAGACGCAGAGATTCT 198
   |||::|||
190  MetGluPhcCysAlaGlnGlyGlnLeuTyrGluValLeuArgAlaGlyArg-----206
   |||::|||
199  TCCTTTATACCCCTGGGACACATGCTCACCCAAAATAGCTACCATCGCTCCGGC 258
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207  -----ProValThrProSerLeuLeuValAspTrpSerMetGlyILeAlaGly 223
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259  CTGGCTTACTGCACAAGAAAAATCATCTTCTGTGACCTCAAGTCGGACAACTTCG 318
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224  MetAsnTyrLeuHisLeuHisILeILeHisArgASPLeuLysSerProAsnMetLeu 243
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319  GTGTGTCCTTGAGCTCAAGAGACACATCAACATCAAGCTATCTGACTACGGATTTCG 378
   |||::|||
244  ILethrTyRAspVal-----ValLysILeSerAspPheGlyThrSer 258
   |||::|||
379  AGCGAG---TCATTCCATGAGCGCCCTAGGCGTGGAGGCGACCTCGGTACACGGCC 435
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259  LysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThrValAlaTrpMetAla 278
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436  CAGAGATCAGCGCTCGCATTTGATATGATGAGAAGTAGATATGTTCTCATGGAATG 495
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279  ProGluValILeArgAsnGluProValSerGluLysValAspILeTrpSerPheGlyVal 298
   |||::|||
496  GTGCTCTACGAGTCTGCTCTAGGACAGCGCCT-----528
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299  ValLeuTrpGluLeuLeuThrGlyGluILeProTyLysAspValAspSerSerAlaILe 318
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823  -----TACCGGTGGTGAACACA-----GAG 843

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Qy	895	TGCAGCTCCAGGTCCAGATCCCTGTGCACAGCCAGCAGACCAAGAAATCTACATC	954
Db	474	oHisProSerArgGlyLeuLeuHisGlyAsnThrMetGluLysLeuLeuLysArgAs	494
Qy	955	TACACCTCAAGGCATGTCCCTTAAACACACCCACACCCAGCTTGGATACTCGACT	1014
Db	494	nValProGlnAsnLeuSer-----ProHisSerGlnArgProAspIleLeuLysAl	511
Qy	1015	GTGCTCACCTGCTTCTTGGCCGTGCTGTATTAAAGAAATCTCTACCTGGTCTTAGCG	1074
Db	511	aGluSer-----LeuLeuProLysLeuAspAlaAl	521
Qy	1075	GGCTCTGCCGATGGCTGTGGGTGTGTTCGCGTGGTGCAGGACCCCAAGGACAGC	1134
Db	521	aLeuSerGlyValGlyLeu-----	527
Qy	1135	TGCTCTTACTGCTGCACACACAGCAACAGTCCAAGTTTCAGCATCCGGATGAAGAC	1194
Db	528	-----ProGlyCysProLysAlaProProSer-----ProGlyArgSerArgArgLysTh	545
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Db	545	rArgHisArg-----LysAlaSerAlaLys	553
Qy	1255	TGCTACAGCAATGGCGCGGCTCTGTGCATCGACTGTGCTCCTCGCTGGAGATCTGCAG	1314
Db	553	sGlySerCysGlyAspLeuProGlyLeuArgThrAlaValProProHisGluProGlyG	573
Qy	1315	CGGCTGGAGCCCT-----ACATGGCCC-----CCTCCCATG	1344
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Qy	1345	GTTACGT-----CA	1353
Db	593	aLeuArgGlyLeuHisAspLeuLeuArgLysMetSerSerSerProAspLys	613
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Db	613	uLeuSerAlaAlaLeuLysSerArgGlyAlaThrGlyAlaGlyAspProG	633
Qy	1408	AGGCGCACTCTGTGTGATGATACACTCCACCACTACCACTGTGTGCCGTACTTC	1467
Db	633	ySerProProAlaArgGlyAspThrProProSerGluGlySerAlaProGlySerTh	653
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Db	708	AlaValThrArgSerGlnLysArgGlyIleSerSerGluGluGluGluGlyValAsp	727
Qy	1579	GGGAGCTGAGCATGATGATGAGAGGTGGCAGCGAGATCTCTGATCCACCGAAG	1638
Db	728	SerGluValGluLeuThr-SerSerGlnArgTrpProGlnSerLeuAsnMetArgGln---	746
Qy	1639	TCACTCACTGACTGTCTCATGTGCTCTCTACTCTCTCATCCCAACCCCGCAGGCTGCC	1698





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nucleic - nucleic search, using sw model

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l number of hits satisfying chosen parameters: 4403344

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Maximum Match 100%

Listing first 45 summaries

base : Published Applications NA:\*

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- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

lc	Score	Match	Length	DB	ID	Description
1	2184	100.0	3496	10	US-09-836-392-8	Sequence 8, Appli
2	1936.8	88.7	7015	15	US-10-132-382-5	Sequence 5, Appli
3	1936.8	88.7	7093	15	US-10-132-382-1	Sequence 1, Appli
4	1936.8	88.7	7229	15	US-10-132-382-7	Sequence 7, Appli
5	1936.8	88.7	7307	15	US-10-132-382-3	Sequence 3, Appli
6	1840	84.2	3112	13	US-10-094-749-50	Sequence 50, Appli
7	477.6	21.9	526	15	US-10-121-925-10	Sequence 10, Appli
8	64.2	2.9	1497	15	US-10-156-761-4356	Sequence 4356, Ap
9	64.2	2.9	9025608	15	US-10-156-761-1	Sequence 1, Appli
10	57.4	2.6	515	15	US-10-101-4648-149	Sequence 149, App
11	55	2.5	2218	13	US-09-820-790-1	Sequence 1, Appli
12	54.6	2.5	1825	13	US-09-820-790-1	Sequence 321, App
13	54.2	2.5	1383	11	US-09-935-464-2	Sequence 2, Appli
14	54.2	2.5	1383	15	US-10-125-835-2	Sequence 2, Appli
15	54.2	2.5	1738	11	US-09-935-464-4	Sequence 4, Appli

# ALIGNMENTS

## RESULT 1

US-09-836-392-8  
; Sequence 8, Application US/09836392  
; Patent No. US20020173458A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides,  
; FILE REFERENCE: PT020P1  
; CURRENT APPLICATION NUMBER: US/09/836,392  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: PCT/US00/28066  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: 60/159,542  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: 60/165,914  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/189,027  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 3496  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-836-392-8

Query Match 100.0%; Score 2184; DB 10; Length 3496;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 22 ATGCTGAGGACCTGGGCGCCACCGATGCGATGAGAACTTCTCCGAGTCCGGCAGGAG 81  
QY 61 GCCAGCATGCTGCACGCGTGCAGACCCCTGATCGTGGCGCTCATCGGCATCAGCATC 120  
DB 82 GCCAGCATGCTGCACGCGTGCAGACCCCTGATCGTGGCGCTCATCGGCATCAGCATC 141



## GENERAL INFORMATION:

APPLICANT: WEISS, BERTRAM  
 TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS

FILE REFERENCE: SCH-1811

CURRENT APPLICATION NUMBER: US/10/132,382

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

EQ ID NO 5

LENGTH: 7015

TYPE: DNA

ORGANISM: Homo sapiens

10-132-382-5

Query Match 88.7%; Score 1936.8; DB 15; Length 7015;

est Local Similarity 94.6%; Pred. No. 0;

atches 2065; Conservative 0; Mismatches 2; Indels 117; Gaps 1;

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61 GCCAGCATGCTGCACGCGCTGCAGCACCCCTCATCGTGGCGCTCATCGGCATCAGCATC 120

4184 GCCAGCATGCTGCACGCGCTGCAGCACCCCTCATCGTGGCGCTCATCGGCATCAGCATC 4243

121 CACCGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 180

4244 CACCGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 4303

181 GAGAACGCCAGAGATTCCTCTTTATACCCCTGGGACACATGCTCACCCAAAAATAGCC 240

4304 GAGAACGCCAGAGATTCCTCTTTATACCCCTGGGACACATGCTCACCCAAAAATAGCC 4363

241 TACAGATCGCTCGGGCTGGCGCTACCTGTCACCAAGAAACATCATCTTCTGTGACCTG 300

4364 TACAGATCGCTCGGGCTGGCGCTACCTGTCACCAAGAAACATCATCTTCTGTGACCTG 4423

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4424 AGTCGGACAACATTCCTGTGTGTCCTTGACGTCAAGAGGACATCAACATCAAGCTA 4483

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4484 TCTGATACGGATTCGAGGACAGTCATTCATGAGGCGCCCTAGGCGTGAGGGCACT 4543

421 CTTGGTACACGCCCCAGATCAGGCTCGCATTTGATATGATGAGAGGTAGATG 480

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QY 1441 ACCTACAGTGTGTGCGGCTTCTTGTGGGGTCCCGAGCGGCTCTGAGGACATGTTT 1500

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DB 5687 CCACCGCGGCGGCTGCGGCTCCCGCTCAAGGCTCCCGAGCTCCCGAGCAAGTCTCTTCC 5746

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DB 5747 AGTGTGCTTCTTCCACGCTGCGGAGCTACAGATGCTACATAGCGGCGGCTGTGCG 5806

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DB 5807 TCCACAGGCTGTGAGCATGACCTGACCCCGATGCGGAGACCTTTCAGCCAGCACCTG 5866

QY 1861 CAGCCGTGAAGATCTCTGCGGCTCAGAGACCTCATTTGGGTCCCGAGCGGCGGCTGGAGAT 1920

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JLT 3  
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 sequence 1, Application US/10132382  
 Application No. US20030045699A1  
 SERIAL INFORMATION:  
 APPLICANT: WEISS, BERTRAM  
 TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS  
 FILE REFERENCE: SCH-1811  
 CURRENT APPLICATION NUMBER: US/10/132,382  
 CURRENT FILING DATE: 2002-04-26  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 7093  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 10-132-382-1

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 1st Local Similarity 94.6%; Pred No. 0;  
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2161 GAGGCTTGACCTGCAAGAGAGG 2184  
6245 GAGGCTTGACCTGCAAGAGAGG 6268

0-132-382-7  
Sequence 7, Application US/10132382  
Publication No. US20030045699A1  
PUBLICATION INFORMATION:  
PUBLICATION: WEISS, BERTRAM  
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS  
FILE REFERENCE: SCH-1811  
PUBLICATION NUMBER: US/10132,382  
PUBLICATION DATE: 2002-04-26  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patent In Ver. 2.1  
Q ID NO 7  
LENGTH: 7229  
TYPE: DNA  
ORGANISM: Homo sapiens  
0-132-382-7

ery Match 88.7%; Score 1936.8; DB 15; Length 7229;  
st Local Similarity 94.6%; Pred. No. 0;  
tches 2065; Conservative 0; Mismatches 2; Indels 117; Gaps 1;  
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Db 6459 GAGGCTTGCACTCGCAAGAGAGG 6482

## RESULT 6

US-10-094-749-50  
; Sequence 50, Application US/10094749  
; Publication No. US20030219741A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMBECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOHICO  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOTYUKI  
; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASUHO, YASUHIKO  
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA  
; FILE REFERENCE: 084335/0160  
; CURRENT APPLICATION NUMBER: US/10/094,749  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/350,435  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: JP 2001-328381  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 3381  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 3112  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-094-749-50

Query Match 84.2%; Score 1840; Length 3112;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1851; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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Db 1 CTTCAAGGAGCACATCAACATCAAGCTATCTGACTAGCGGATTTGAGGAGTCATTCCA 60  
Qy 393 TGAGGGCGCCCTAGGCGTGGAGGCACTCTGCTACCAAGGCCCAAGAGATCAGGCTCG 452  
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1533	Qy	AGCCAGCCAC	CHAGGCC	CHACCC	AAAGTG	GCTT	GAGGG	AGACT	CCAT	TCGG	AGCG	CTG	AGCAT	1592
1201	Db	AGCCAGCCACA	CGGCC	CAACCC	AAAGTG	GCTT	GAGGG	AGACT	CCAT	TCGG	AGCG	CTG	AGCAT	1260
1593	Qy	CATGTACAGT	GAGGAG	CTGGG	CACG	CAGAT	CTCT	GTATCC	AC	CAGGA	ATCA	CTCA	CTGACTA	1652
1261	Db	CATGTACAGT	GAGGAG	CTGGG	CACG	CAGAT	CTCT	GTATCC	AC	CAGGA	ATCA	CTCA	CTGACTA	1320
1653	Qy	CTGTCCCATG	TCCTT	CTTACT	TCCTT	CA	TCC	CCAC	CCCG	CCAG	GCTT	GC	CAGGTT	1712
1321	Db	CTGTCTCATG	TCCTT	CTTACT	TCCTT	CA	TCC	CCAC	CCCG	CCAG	GCTT	GC	CAGGTT	1380
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1773	Qy	AGACATGCTA	CATACG	CCCG	CGT	CGCT	CC	CAG	AGT	CT	GT	GAG	CATG	1832
1441	Db	AGACATGCTA	CATACG	CCCG	CGT	CGCT	CC	CAG	AGT	CT	GT	GAG	CATG	1500
1833	Qy	GGACGGGAG	AC	TTT	CAG	CAG	CAC	CTG	CAG	GGC	CGT	GA	AGAT	1892
1501	Db	GGACGGGAG	AC	TTT	CAG	CAG	CAC	CTG	CAG	GGC	CGT	GA	AGAT	1560
1893	Qy	CATTTGGGT	CCCC	CAGG	CGG	CGT	GG	AGAT	GT	TAT	CGT	CA	T	1952
1561	Db	CATTTGGGT	CCCC	CAGG	CGG	CGT	GG	AGAT	GT	TAT	CGT	CA	T	1619
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2013	Qy	GCTGTGGAT	GCT	CGCT	TGGT	TGG	CA	AA	GAG	CA	CT	GT	TGT	2072
1680	Db	GCTGTGGAT	GCT	CGCT	TGGT	TGG	CA	AA	GAG	CA	CT	GT	TGT	1739
2073	Qy	CACAGAT	GTTG	TCCT	TGG	CCGT	CT	GT	GAG	GGG	CT	GGG	CGC	2132
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## RESIN, T 7

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RESULTS
US-10-121-925-10
Publication 10, Application US/10121925
Publication No. US20030104505A1
GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
FILE REFERENCE: MNI-090
CURRENT APPLICATION NUMBER: US/10/121,925
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/09/948,802
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO. 10
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-10-121-925-10

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Query Match 21.9%; Score 477.6; DB 15; Length 526;  
Best Local Similarity 98.5%; Pred. No. 2.1e-124;  
Matches 513; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

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181	GTCAAGACAGCGCCTGCACCTGGGCGACCA	240
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993	ACAGGCTTGGATACTCCAGCTGTCTGTACCTGCTTCTTGCCGCTGCTGTATTAAAAA	1052
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721	GAATTCCTACCTGGTCTTAGCGGGCCTCCGATGGGCTTGTGCGCTGTGTTCCGNGGT	780
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781	CGGGGACCCCCAAAGGACAGCTGCTCTACTGTGCTCACACAGCACCAACAGGTCCTAA	840
1173	GTTCAAGCATCCGCGATGAAGACGCAAGGACAGCCCTACCCAGTGAAGCCATGAGGT	1232
841	GTTCAAGCATCCGCGATGAAGACGCAAGGACAGCCCTACCCAGTGAAGCCATGAGGT	900
1233	GGTCAACAGCGGCTCTGAGTCTGTGTACAGCAATGGGCGCGGCTCTTGTTCATCGACTG	1292
901	GGTCAACAGCGGCTCTGAGTCTGTGTACAGCAATGGGCGCGGCTCTTGTTCATCGACTG	960
1293	TGCTTCCTGGAGATCTGACGGCGGCTGGAGCCCTACATGGCCCTCCATGGTTAGTCT	1352
961	TGCTTCCTGGAGATCTGACGGCGGCTGGAGCCCTACATGGCCCTCCATGGTTAGTCT	1020
1353	AGTCGTGTGACGCTCTCAGGGGACAGGGGAGGAGGTGCTGTGGTGCCTGGATGACAAGGC	1412
1021	AGTCGTGTGACGCTCTCAGGGGACAGGGGAGGAGGTGCTGTGGTGCCTGGATGACAAGGC	1080
1413	CAACTCTTGGTGTATGATACCTCCACCTACAGCTGTGCGCGGCTACTTCTCGG	1472
1081	CAACTCTTGGTGTATGATACCTCCACCTACAGCTGTGCGCGGCTACTTCTCGG	1140
1473	GGTCCCCAGCCCCCTCAGGACATGTTTCCGTGGCGCCCTTGGACACGGAACCCCGGC	1532
1141	GGTCCCCAGCCCCCTCAGGACATGTTTCCGTGGCGCCCTTGGACACGGAACCCCGGC	1200

289 TTCTGTGACCTGAAGTCGACCAACATCTCGTGGTCCCTTGCAGCTCAAGGAGCACATC 348  
6 TCCGGTGAACCTGAAGTCGACCAACATCTCGTGGTCCCTTGCAGCTCAAGGAGCACATC 65  
349 AACATCAAGCTATCTGACTACGGGATTCAGGAGCTATTCATGAGGCGCCCTAGGC 408  
66 AACATCAAGCTATCTGACTACGGGATTCAGGAGCTATTCATGAGGCGCCCTAGGC 125  
409 GTGAGGCGCTCTCTGCTACGAGCCAGGCGCCAGAGATCAGGCTCGCATTTATATGATGAG 468  
126 GTGAGGCGCTCTCTGCTACGAGCCAGGCGCCAGAGATCAGGCTCGCATTTATATGATGAG 185  
469 AAGTAGATATGTTCTCTTATGGAATGGTCTCTACGAGTTGCTGTCAGGACAGCGCCCT 528  
186 AAGTAGATATGTTCTCTTATGGAATGGTCTCTACGAGTTGCTGTCAGGACAGCGCCCT 245  
529 GCATGAGGCGCTCTCTGCTACGAGCTCGAGATTCGAGAGCTGTCGAGGCGATTCGCGCGTT 588  
246 GCATGAGGCGCTCTCTGCTACGAGCTCGAGATTCGAGAGCTGTCGAGGCGATTCGCGCGTT 305  
589 CTGGGCGAGCGGAGGAGGAGTGCAGTTCCGCGGAGTGCAGGCGCTCATGATGAGTGTGG 648  
306 CTGGGCGAGCGGAGGAGGAGTGCAGTTCCGCGGAGTGCAGGCGCTCATGATGAGTGTGG 365  
649 GACACTAAGCCAGAGAGGAGCGCTGCGGCGCTGTCGTTGGT-AGCCAGATGAAGGACCC 707  
366 GACACTAAGCCAGAGAGGAGCGCTGCGGCGCTGTCGTTGGTGAAGCCAGATGAAGGACCC 425  
708 GACTTTTGCACCTTCATGATGAGTGCAGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 766  
426 GACTTTTGCACCTTCATGATGAGTGCAGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 485  
767 CCAGGCGCAGGAGTACACCGT-GGTGTTTGGGATGGAAA 806  
486 NCCAGGCGCAGGAGTACACTGTGGGTGTTTGGGATGGAAA 526

## LT 8

10-156-761-4356  
Sequence 4356, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
Q ID NO 4356  
LENGTH: 1497  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1497)  
0-156-761-4356

ery Match 2.9%; Score 64.2; DB 15; Length 1497;  
st Local Similarity 43.4%; Pred No. 1.1e-07;  
tches 294; Conservative 0; Mismatches 383; Indels 0; Gaps 0;  
23 CCGATGCCATGAAGAACTTCTCCGAGTTCCGGCAGGAGCGCCAGCATGCTGCAGCGCTGC 82

164 CCAGGAGCCCGGTCTCCAAAGGCCCGCTTCAACGCGGAGGCGCCAGTCGGTGGCGGCTCA 223  
83 AGCACCCCTGCTATCGTGGCGCTCATCGGCATCAGCATCCACCGGCTCTGCTTCGGCCCTGG 142  
224 ACACCATCGGCTGCTGGCGGTGTAGGACTCCGGGAGAGACGTCGTCGGGCACTCCACCG 283  
143 AGTCGCGCGGCTCAGCAGCCTCAACACCGTCTCTCCGAGAACGCCAGAGATTCTTCT 202  
284 TCCGCTACATCGTGTGAGCTGGTCGAGGGCGCACCATCCGCGACCTGCTGTCTCAACG 343  
203 TTATACCCCTGGGACACATGCTCACCCAAAATAGCTACCATCCGCTCGGSCCTGG 262  
344 CGAGGCCCGGGGCCGAGCAGGCTTATCATGCTCTCCGGGTGCTGGAGGCGCTGG 403  
263 CTACCTGACCAAGAAAACATCATCTTCTGTGACCTCAAGTCGGACAACTTCTGGTGT 322  
404 CTTACTCGCACGACGAGCATCTGTCACCGGACATCAAGCGGCGCAACGTCATCATCA 463  
323 GGTCCCTTACCTCAGGAGGACATCAACATCAAGCTATCTGACTACGGGATTTGGAGGC 382  
464 CGACAAACGCTGCCGTGAAGTTCATGACCTTCGGCATCGCGCGGCGCTGCACGCGCGC 523  
383 AGTCATTCATGAGGCGCGCTTAGCGGTGGAGGCGACCTCTGGTACCGAGGCCAGAGA 442  
524 AGTCGAGCATGACGAGACCGGCTGTCATGGGACCGCCGACGATCTGTCCGCCGAGC 583  
443 TCAGGCGCTGCGATTTATATGATGAGAGGTAGATATGTTCTCTTATGGAATGGTGTCT 502  
584 AGCGCTCGGAAAGCGGTGCGACACCGCAGCGACCTGTACCGACCGTTGCTGTCTCT 643  
503 ACGAGTGTGCTGCAGGACAGCGCCTGCACCTGGGCGCCACCGAGCTCCAGATTCGCAAGA 562  
644 ACGAACTCTGCGCTGCGGCGCCCGTTCCCGGTGAGACCGCGCTCTCCGTGTCTTACC 703  
563 AGCTTCCAAAGGCGATCCGCGCGTCTTGGGCGCAGCGGAGGAGTGCAGTCCGCGGAC 622  
704 AGCAGTGCAGGACATCCGCTGCCCGTCCGAGGTCCGGAAGGGCGCCGCGGAGC 763  
623 TCGAGGCGCTCATGATGAGTGTGCGGACACTAAGCCAGAGAGCGGACCGCTGCGCCCTGT 682  
764 TCGAGGACTCGTGTGATGCGTCTCGGAGGATCCCGACGACCGGTTCCAGACCGCG 823  
683 CGTGGTGCAGCGCATG 699  
824 AGGAGATCGCGGCGTG 840

## RESULT 9

US-10-156-761-1  
Sequence 1, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 1  
LENGTH: 9025608  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis

FEATURE:

NAME/KEY: misc feature  
LOCATION: (4187715)  
OTHER INFORMATION: a, t, c, g, other or unknown  
10-156-761-1  
Query Match 2.9%; Score 64.2; DB 15; Length 9025608;  
Best Local Similarity 43.4%; Pred. No. 1.4e-06;  
Matches 294; Conservative 0; Mismatches 383; Indels 0; Gaps 0;  
23 CCGATGCGCATGAAGAACTTCTCCGAGTTCCGGCAGGAGCCAGCATGTCGACGGGCTGC 82  
5351896 CCGAGGACCGGTCTCCAGGCCCGCTTACGGCGGAGGCCAGTCGGTGGCGGGCTCA 5351955  
83 AGACCCCTGCATCGTGGCGCTCATCGGCATAGCATCCACCGCTCTGCTTCGCGCTGG 142  
5351956 ACCACCATGGGTGCTGCGCGTGTAGCACTCCGGCGAGGACGTCGTCGGGCACTCCACG 5352015  
143 AGCTCGCGCGCTCAGCAGCTCAACACCGTGTGTCGAGAACCCAGAGATTCTTCT 202  
5352016 TCCGTATCATGTGATGGAGCTGTCGAGGGCGGCACCATCCCGACCTGCTGCTCAACG 5352075  
203 TTATACCCCTGGGACATGCTCACCACCAAAATAGCTTACAGATCGCTCGGGCTGG 262  
5352076 CCGAGGCCCGGGCGCGAGCAGCGCTTATCATGCTCTCCGGGTGCTGGAGGCGCTGG 5352135  
263 CCTACCTGCACAGAAACATCATCTTCTGTGACCTGAAGTCGACACAACTTGTGTGT 322  
5352136 CCTACTCGCACAGCAGGATCGTGCACCGGACATCAAGCCGCCAACGTCATCA 5352195  
323 GGTCCCTTACGTCACAGGAGCACAATCAACATCAAGCTATCTGACTACGGGATTTGAGGC 382  
5352196 CGCACACGGTGCCTGAAGTCTATGACTTCGGCATCGCGCGCCCTCGACGGCGCG 5352255  
383 AGTCATTCCATGAGGGCGCTTAGGGCTGGAGGCACTCTGGCTTACAGGCCCGCCAGAGA 442  
5352256 AGTCGACGATGACCGAGACCGGATGTCATGGCAGCGCGAGTACCTGTCGCCCGAGC 5352315  
443 TCAGGCTCTCATTTATATGATGAGAAGGTAGATATGTCCTCATGGAATGTGCTCT 502  
5352316 AGCGCTCGGAAGCGGTGCGACCCAGCGAGCTGTACCGGACCGGTGCTGCTCT 5352375  
503 ACAGATGCTGTGACGACAGCGCTTACGCTGCGGACACACAGCTCCAGATTGCCAAGA 562  
5352376 ACAGATCTCTCGCGCTGCGGCGCCCGCTTACCGGTGAGACCCCGCTGCTGCTTACC 5352435  
563 AGCTGTCCAGGSCATCCCGGCTTCTGGGCGACCGGAGAGTGAGTTCGGCGAC 622  
5352436 AGACGTGACGACATCCCGGTGCCCCCTCCGAGGTCCGGAAGGGCGCGCGCGAGC 5352495  
623 TGCAGGCGCTCATGATGAGTGTGGGACACTAAGCCAGAGAGCGACCGTGGCCCTGT 682  
5352496 TCGACGAGCTCGTGTATGCTGCTCGCTCGGAGGATCCCGACGCGGTTCACAGACCGCG 5352555  
683 CGGTGTGACCCAGATG 699  
5352556 AGGAGATGCGCGGCTG 5352572

LT 10

Sequence 149, Application US/10101464A  
Publication No. US20030046728A1  
GENERAL INFORMATION:  
APPLICANT: Strabala, Timothy  
APPLICANT: Nieuwenhuizen, Nicolaas  
APPLICANT: Higgins, Colleen M.  
TITLE OF INVENTION: Compositions Isolated from Plant Cells  
TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signaling  
FILE REFERENCE: 11000.102062  
CURRENT APPLICATION NUMBER: US/10/101,464A  
PRIORITY FILING DATE: 2002-03-18  
PRIORITY APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 09/228,986  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/162,866  
PRIOR FILING DATE: 1999-11-01  
PRIOR APPLICATION NUMBER: PCT/US00/00724  
PRIOR FILING DATE: 2000-01-11  
NUMBER OF SEQ ID NOS: 989  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 149  
LENGTH: 515  
TYPE: DNA  
ORGANISM: Eucalyptus grandis  
US-101-464A-149

Query Match 2.6%; Score 57.4; DB 15; Length 515;  
Best Local Similarity 51.8%; Pred. No. 7e-06;  
Matches 130; Conservative 0; Mismatches 121; Indels 0; Gaps 0;  
QY 273 CAAAGAAAACATCATCTTCTGTGACCTGAAGTCGGACAAATCTGTGTGGTCCCTTGA 332  
Db 58 CAAGCAGACCATATTATACACCGCGACATGAGACCAACCAATCTGCTCGACGAGAAGTG 117  
QY 333 CQTCAAGGAGCACAATCAACATCAAGCTATCTGACTACGGGATTTTCGAGGCGATCATTTCCA 392  
Db 118 GGTTCGCAAGGTGTCGGAATTCGGGCTCTCGAAGTTCGGCCGACGTCGGTGTCCAAGGC 177  
QY 393 TGAGGCGCCCTTAGCGGTGGAGGCACTCTCTGGTACAGGCCCGCCAGAGATCAGGCGCTCG 452  
Db 178 CCACGTCAGCACCGGTGTGAAGGCGACCTTCGGGTACTCTGGATCCAGAGTACTACAGGCG 237  
QY 453 CATTTGATATGATGAGAAGTAGATATGTTCTCTATGGAATGCTCTTACGAGTTGCT 512  
Db 238 CCAGCAGTGAAGTGAAGTCCGACGTCGACGTCGTCCTTCGGGTGCTTATTCGAGGTGCT 297  
QY 513 GTCAGGACAGC 523  
Db 298 GTGTGCAAGGC 308

RESULT 11

US-09-820-790-1  
Sequence 1, Application US/09820790  
Publication No. US20030140354A1  
GENERAL INFORMATION:  
APPLICANT: SHAO, Wei et al.  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: CL001204  
CURRENT APPLICATION NUMBER: US/09/820,790  
CURRENT FILING DATE: 2001-03-30  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2218  
TYPE: DNA  
ORGANISM: Human  
US-09-820-790-1

Query Match 2.5%; Score 55; DB 13; Length 2218;  
Best Local Similarity 48.0%; Pred. No. 5.1e-05;  
Matches 157; Conservative 0; Mismatches 170; Indels 0; Gaps 0;  
QY 240 CTACAGATCGCTCGGCGCTTACCTGCAAGAAAAACATCATCTTCTGTGACCT 299  
Db 612 CCAGCAGATCTCGAGCGCTTCTCCATTGTCACCAATGGGGTCTCCACAGACCT 671  
QY 300 GAAGTCGACAAATTCGTGTGGTCCCTTGGAGTCGTCAGGAGCAGATCAACATCAAGCT 359  
Db 672 CAAAGCCGAGAACCTGCTTCTGCGCAGCAAGTGAAGGGGCTGCACTGAAGCTGGCAGA 731  
QY 360 ATCTGACTACGGGATTTTCGAGGCGAGTCATTCATGAGGCGCCCTAGGCGTGGAGGCGAC 419

732 CTTGGCCTAGCTATCGAGGTGCGAGGGGACACAGGCGCATGGTTTGGTTGGCTGGCAC 791  
420 TCTCGCTACAGGCGCCAGAGATCAGCCCTCGCATTTATATGATCAGAGGTAGATAT 479  
792 ACCAGGCTACCTGTCCCTCGAGTCTTCCGAAGAGCGGTATGGCAAGCTGTGGACAT 851  
480 GTTCTCCTATGAATGGTGCTCTACAGTCTGTCTCAGGACAGCGCCCTGCACCTGGGCCA 539  
852 CTGGCAGTGTGGGTGATCCCTGTACATCTCTGTGGCTACCCACCTTCTGGGACGA 911  
540 CCACAGCTCCAGATGCGCAAGACT 566  
912 GGACAGCACAAGCTGTACCAAGCAGAT 938

LT 12  
0-116-275-321  
Sequence 321, Application US/10116275  
Publication No. US20030211476A1  
GENERAL INFORMATION:  
APPLICANT: Elan Pharmaceutical Technology  
APPLICANT: O'Mahony, Daniel J.  
APPLICANT: Brayden, David  
APPLICANT: Byrne, Daragh  
APPLICANT: Lambkin, Imelda  
APPLICANT: Higgins, Lisa  
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and  
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors  
FILE REFERENCE: E1067/20087  
CURRENT APPLICATION NUMBER: US/10/116,275  
CURRENT FILING DATE: 2002-10-04  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 321  
LENGTH: 1825  
TYPE: DNA  
ORGANISM: Homo sapiens  
0-116-275-321

Query Match 2.5%; Score 54.6; DB 13; Length 1825;  
Best Local Similarity 47.7%; Pred. No. 6.2e-05;  
Matches 156; Conservative 1; Mismatches 170; Indels 0; Gaps 0;

240 CTACAGATCGCTCGGGCTGGCTACCTGACAGCAAGAAACATCATCTTCTGTGACCT 299  
397 CAGCAGATCTGTGAGGCGCTTCTCATTTGTCCAAATGGGGTGTCTCCACAGACCT 456  
300 GAAGTCGACAAACATTTCTGGTGTGCTTGCCTTGCCTCAAGGAGCACATCAACATCAAGCT 359  
457 CAAGCGGAGAACCTGCTTCTGGCCAGCAAGTGCAAGGGGCTGCAGTGAAGCTGGCAGA 516  
360 ATCTGACTACGGGATTCAGGCGCTCATTCATGAGGCGCCCTAGCGTGGAGGCGAC 419  
517 CTTCGGCCTAGCTATCGAGGTGCGGGGACACAGGCGCATGGTTGGTTTGGCTGGCAC 576  
420 TCTGTCTACAGGCGCCAGAGATCAGGCTCGCATTTATATGATCAGAGGTAGATAT 479  
577 ACCAGCTACCTGTCCCTGAGTCTTCCGAAGAGCGGTACGCGAAGCCGCTGGACAT 636  
480 GTTCTCCTATGAATGGTGCTCTACAGTGTGCTGTCAGGACAGCGCCCTGCACCTGGGCCA 539  
637 CTGGGATGTGGGGTATCCTGTACATCTCTGTGGCTACCCACCTTCTGGGACGA 696  
540 CCACAGCTCCAGATGCGCAAGACT 566  
697 GGACAGCACAAGCTGTACCAAGCAGAT 723

GENERAL INFORMATION:  
APPLICANT: Meyer, Joanne  
APPLICANT: Barrington-Martin, Rory  
APPLICANT: Parker, Alexander  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHI  
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA  
FILE REFERENCE: 3322/1H702 US1  
CURRENT APPLICATION NUMBER: US/09/935,464  
CURRENT FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: US 09/757,300  
PRIOR FILING DATE: 2001-01-09  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 1383  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-935-464-2

Query Match 2.5%; Score 54.2; DB 11; Length 1383;  
Best Local Similarity 49.9%; Pred. No. 7.4e-05;  
Matches 168; Conservative 0; Mismatches 163; Indels 6; Gaps 1;

QY 240 CTACAGATCGCTCGGGCTGGCTACCTGACAGCAAGAAACATCATCTTCTGTGACCT 299  
DB 372 CAGCAGGTCTTGTGGCAGTGAATACCTACATGAGATGGCATGTCACAGACATT 431  
QY 300 GAAGTCGACAAACATTTCTGGTGTGCTTGCCTTGCCTCAAGGAGCACATCAACATCAAGCT 359  
DB 432 AAAGCCGCAAAACCTGCT-----TTACCTTACCCCTGAAGAGAACTCTAAGATCATGAT 485  
QY 360 ATCTGACTACGGGATTTTCAGGCGCTCATTCCTCAGGCGCCCTAGGCGTGGAGGCGAC 419  
DB 486 CACTGACTTTGCTGTCCAGATGGAACAGATGGCATGTCTCACTGCTGTGGAC 545  
QY 420 TCTGTCTACAGGCGCCAGAGATCAGGCTCGCATTTGATATGATCAGAGGTAGATAT 479  
DB 546 CCCAGGCTACGTGGCTCCAGAAGTGTGGCCAGAACCCCTACAGCAAGCTGTGGATTG 605  
QY 480 GTTCTCCTATGAATGGTGCTCTACAGTGTGCTGTCAGGAGTGTGTCAGGACGCGCCCTGCACCTGGGCCA 539  
DB 606 CTGGTCCATCGCGCTCATCCTACATATTGCTCTGTGGATACCCCCCATTTCTATGAAGA 665  
QY 540 CCACAGCTCCAGATGCGCAAGAGCTGTCCAAAGGGC 576  
DB 666 AACGAGTCTAAGCTTTTCGAGAGATCAAGAGGGC 702

RESULT 14  
US-10-125-835-2  
Sequence 2, Application US/10125835  
Publication No. US20030092019A1  
GENERAL INFORMATION:  
APPLICANT: Meyer, Joanne  
APPLICANT: Barrington-Martin, Rory  
APPLICANT: Parker, Alexander  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING  
TITLE OF INVENTION: NEUROPSYCHIATRIC  
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA  
FILE REFERENCE: 3322/0H702 US0  
CURRENT APPLICATION NUMBER: US/10/125,835  
CURRENT FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: US/09/757,300  
PRIOR FILING DATE: 2001-01-09  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 1383  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-125-835-2

Query Match 2.5%; Score 54.2; DB 15; Length 1383;

est Local Similarity 49.9%; Pred. No. 7.4e-05; matches 168; Conservative 0; Mismatches 163; Indels 6; Gaps 1;

240 CTACAGATCGCCTCGGCGCTGACCTGACAGAAACATCATCTTCTGTGACCT 299

372 CCAGCAGGCTTTCGCGCAGTGAATACCTATGAGAAATGGCATCGTCCACAGAGACTT 431

300 GAAGTCGGACAAATCTGTGTGTGTCCTTACGCTGACGAGCAGATCAACATCAAGCT 359

432 AAAGCCGAAACCTGCT-----TTACCTTACCCCTGAAGAGAACTCTAAGATCATGAT 485

360 ATCTGACTACGGGATTTGAGGAGTCATCTCCATGAGGCGCCCTAGCGGTGGAGGCAC 419

486 CACTGACTTTTGGTCTGTGCCAAGATGAACAGAAATGGCATCATGTCCACTGCTGTGGAC 545

420 TCTGTGCTACAGGCCCCAGAGATCAGGCTGCGATTGTATGATGAGAAGGTAGATAT 479

546 CCCAGGCTAGTGGCTCCAGAGTGTGGCCAGAAACCTACAGCAGGCTGTGGATTG 605

480 GTTCTCCTATGGAATGGTGTCTACAGATGTGTGTCAGACAGCGCCCTGCACTGGGCCA 539

606 CTGTCATCGGGCTCATACCTACATATTGCTCTGTGGATACCCCCCATTTCTATGAAGA 665

540 CCACGAGCTCCAGATGCCAAGAAGCTGTCCAGGGC 576

666 AACGGAGCTTAAGCTTTTCGAGAAGATCAAGGAGGC 702

Search completed: December 14, 2003, 06:55:23

Job time : 7.0 secs

ULT 15

09-935-464-4

sequence 4, Application US/05935464

ublication No. US20030027153A1

GENERAL INFORMATION:

APPLICANT: Meyer, Joanne

APPLICANT: Barrington-Martin, Rory

APPLICANT: Parker, Alexander

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA

TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA

FILE REFERENCE: 3322/1H702 US1

CURRENT APPLICATION NUMBER: US/09/935,464

CURRENT FILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: US 09/757,300

PRIOR FILING DATE: 2001-01-09

NUMBER OF SEQ ID NOS: 90

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 1738

TYPE: DNA

ORGANISM: Homo sapiens

09-935-464-4

Query Match

est Local Similarity 49.9%; Pred. No. 7.9e-05; matches 168; Conservative 0; Mismatches 163; Indels 6; Gaps 1;

240 CTACAGATCGCCTCGGCGCTGACCTGACAGAAACATCATCTTCTGTGACCT 299

389 CCAGCAGGCTTTCGCGCAGTGAATACCTACATGAGATGGCATCGTCCACAGAGACTT 448

300 GAAGTCGGACAAATCTGTGTGTGTCCTTACGCTGACGAGCAGATCAACATCAAGCT 359

449 AAAGCCGAAACCTGCT-----TTACCTTACCCCTGAAGAGAACTCTAAGATCATGAT 502

360 ATCTGACTACGGGATTTGAGGAGTCATCTCCATGAGGCGCCCTAGGGGTGGAGGCAC 419

503 CACTGACTTTGGTCTGTCCAGATGGAACAGATGGCATCATGTCCACTGCCCTGTGGGAC 562

420 TCTGGCTACAGGCGCCAGAGATCAGGCTCGCATTTGTATGATGAGAAGGTAGATAT 479

563 CCCAGGCTACGTGGCTCCAGAAAGTGTGGCCAGAAACCCCTACAGCAAGGCTGTGGATTG 622

480 GTTCTCCTATGGAATGGTGTCTACGAGTTGCTGTACGAGTCAGGCGCCCTGCACTGGGCCA 539